

Alignment 1

Alignment Report of Unfiled ClustalV (Weighted)

Friday, September 05, 2003 9:42 AM

... . C G . G . A G G C A T C T . C T . G G . . A A G C A A . T Consensus #1
G C A C G C G A G X A G G C A T C T X C T T G C G G G G A A A A G G T G C A A X T Majority

	170	180	190	200	
161	G C C C G C G A G	G A G G C A T C T	T C T T G C C G G G G	G A A G G C C C A A T	T 43030 16s
138	A T A C A C G G T	A G G C A T C T	A C T T G T G T G	A A A G A T G C C A A C	T 49025 16s
159	G C A - G C G A G	C A G G C A T C T	G C T C G C T G G G	A A A G G T G C C A A G	T 49029 16s

G . . . C G C . G A . . G A G G A G C C C G C G C G C A T T A G C T . G T T G Consensus #1
G C A T C G C T G A G A G A G G A G C C C G C G C G C A T T A G C T A G T T G Majority

	210	220	230	240	
201	G G G T C G C T G A G A G A G G A G C C C C G C G C G C A T T A G C T A G T T G	43030 16s			
178	G C A T C G C T G A G A G A G G A G C C C C G C G C G C A T T A G C T A G T T G	49025 16s			
198	G C A C C G C A G A T G A G G A G C C C C G C G C G C A T T A G C T G T T G	49029 16s			

G . G . G G T A A C G G C . C A C C A A G G C G A C G A T G C G T A G C C G A C Consensus #1
G T G G G G T A A C G G C T C A C C A A G G C G A C G A T G C G T A G C C G A C Majority

	250	260	270	280	
241	G C G G G T A A C G G C C A C C C A A G G C G A C G A T G C G T A G C C G A C	43030 16s			
218	G T G A A C G G C T C A C C A A G G C G A C G A T G C G T A G C C G A C	49025 16s			
238	G T G G G T A A C G G C T C A C C A A G G C G A C G A T G C G T A G C C G A C	49029 16s			

C T G A G A G G G T G . . C G G C C A C A C T G G G A C T G A G A C A C G G C C Consensus #1
C T G A G A G G G T G A C C C G G C C A C A C T G G G A C T G A G A C A C G G C C Majority

	290	300	310	320	
281	C T G A G A G G G T G A C C G G C C A C A C T G G G A C T G A G A C A C G G C C	43030 16s			
258	C T G A G A G G G T G A C C G G C C A C A C T G G G A C T G A G A C A C G G C C	49025 16s			
278	C T G A G A G G G T G G A C G G C C A C A C T G G G A C T G A G A C A C G G C C	49029 16s			

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C A G A C T C C T A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A Consensus #1
 C A G A C T C C T A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A Majority

330 340 350 360

321 C A G A C T C C T A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A 43030 16s
 298 C A G A C T C C T A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A 49025 16s
 318 C A G A C T C C T A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A A 49029 16s

T G G G C G C A A G C C C T G A C G G A G C A A C G C C G C G T G A G C G A A G A Consensus #1
 T G G G C G C A A G C C C T G A C G G A G C A A C G C C G C G T G A G C G A A G A Majority

370 380 390 400

361 T G G G C G C A A G C C C T G A C G G A G C C A A C G C C G C G T G A G C G A A G A 43030 16s
 338 T G G G C G C A A G C C C T G A C G G A G C C A A C G C C G C G T G A G C G A A G A 49025 16s
 358 T G G G C G C A A G C C C T G A C G G A G C C A A C G C C G C G T G A G C G A A G A 49029 16s

A G G C C T T C G G G T T G T A A A G C T C . G T . . C T C G G G . A G A G C G Consensus #1
 A G G C C T T C G G G T T G T A A A G C T C T G T T G C T C G G G G A G A G C G Majority

410 420 430 440

401 A G G C C T T C G G G T T G T A A A G C C T C T G T T G C T C G G G G A G A G C G 43030 16s
 378 A G G C C T T C G G G T T G T A A A G C C T C T G T T G C T C G G G G A G A G C G 49025 16s
 398 A G G C C T T C G G G T T G T A A A G C C T C A G T C A C T C G G G A A G A G C G 49029 16s

. C A . G G . G . . T G G A A A G C . C C . T G . G A G A C G G T A C C G A G . Consensus #1
 G C A A G G G A G T G G A A A A G C C C C T T G X G A G A C G G T A C C G A G T Majority

450 460 470 480

441 G C A T G G G G A T G G A A A A G C C C C G T G C G A G A C G G T A C C G A G T 43030 16s
 418 A C A A G G A G A G T G G A A A A G C C T T G T G A G A C G G T A C C G A G T 49025 16s
 438 G C A A G G G A G T G G A A A A G C C C C T T G A G A G A C G G T A C C G A G A 49029 16s

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G A G G A A G C C C C G G C T A A C T A C G T G C C A G C C A G C C G C G G T A A Consensus #1
 G A G G A A G C C C C G G C T A A C T A C G T G C C A G C C A G C C G C G G T A A Majority

481 G A G G A A G C C C C G G C T A A C T A C G T G C C A G C C A G C C G C G G T A A 520 43030 16s
 458 G A G G A A G C C C C G G C T A A C T A C G T G C C A G C C A G C C G C G G T A A 49025 16s
 478 G A G G A A G C C C C G G C T A A C T A C G T G C C A G C C A G C C G C G G T A A 49029 16s

. A C G T A G G G G C . A G C G T T G T C C G G A A T C A C T G G G . C G T A Consensus #1
 T A C G T A G G G G C A A G C G T T G T C C G G A A T C A C T G G G - C G T A Majority

521 A A C G T A G G G G C G A G C G T T G T C C G G A A T C A C T G G G - C G T A 560 43030 16s
 498 T A C G T A G G G G C A A G C G T T G T C C G G A A T C A C T G G G G C G G T A 49025 16s
 518 T A C G T A G G G G C A A G C G T T G T C C G G A A T C A C T G G G - C G T A 49029 16s

A A G . G T G C G T A . G C G G T . G . G . . . G T C . G . . . T G A A A G T C Consensus #1
 A A G C G T G C G T A G G C G G T T G X G T A A G T C T G G A A G T G A A A G T C Majority

570 580 590 600
 560 A A G G T G C G T A G G C G G T C G A G C A A G T C T G G A G T G A A A G T C 43030 16s
 538 A A G C G T G C G T A N G C G G T T G T G T A A G T C T G A C T G A A A G T C 49025 16s
 557 A A G C G T G C G T A G G C G G T T G C G T G T C C G G G T G A A A A G T C 49029 16s

C A . G G C T C . A C C . T G G G . . . G C . T T G G A A A C T G C . T . . A C Consensus #1
 C A X G G C T C A A C C X T G G G A A T G C T T T G G A A A C T G C X T G - A C Majority

610 620 630 640
 600 C A T G G C T C A A C C A T G G G A T G G C T T T G G A A A C T G C T T G - A C 43030 16s
 578 C A A G G C T C N A C C T T G G G N A T G C T T T G G A A A C T G C A T G G A C 49025 16s
 597 C A G G G C T C A A C C C T G G G A A T G C C T T G G A A A C T G C G T A - A C 49029 16s

Alignment 1

1
T T G A G T G C T G G A G A G G C . A G G . . A A T T C C . C G T G T . A . C G Consensus #1
T T G A G T G C T G G A G A G G C A A G G G G A A T T C C X C G T G T - A G C G Majority

639	T	T	G	A	G	T	G	C	T	G	G	A	G	G	C	A	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G			
618	T	T	G	A	G	T	G	C	T	G	G	A	G	G	C	N	A	A	A	T	T	C	C	N	C	G	T	G	T	C	A	C	G	T	G	T	-	A	G	C	G
636	T	T	G	A	G	T	G	C	T	G	G	A	G	G	C	A	A	G	G	G	G	A	A	T	T	C	C	G	C	G	T	G	T	-	A	G	C	G			

G T G . A A . T G C G . . A . A . A T G . G G A G G A A T A C C A G T G G C . A C o n s e n s u s # 1
C T C G Y A A - T G C G T - A G A T A T G T G G A G G A A T A C C A G T G G C G A M a j o r i t y

	690	700	710	720	
678	G T G A A - T G C G T - A G A	A T G T G G A G G A A T A C C A G T G G C G A	43030	16s	
658	G T G N A A A T G C G N T A N A T A T G T G G A G A T A C C A G T G G C N A	49025	16s		
675	G T G G A A - T G C G T - A G A T A T G C G G A G G A A T A C C A G T G G C G A	49029	16s		

A . G C G C C T T . G C C T G G A C A G T G . A C T G A C G C T G A . G G C A C G C C o n s e n s u s # 1
A Y C C C G C C T T - G C C T G G A C A G T G - A C T G A C G C T G A - G G C A C G M a j o r i t y

	730	740	750	760
716	A	R	G	C
698	A	N	G	C
713	A	G	G	C

[illegible]

	770	780	790	800	
753	A A - G C G T G G G G A G C A A	- - - - -	- - - - -	- - - - -	43030 16S
738	A A A A N C G T G G G A N C A A	C N G G A T T A N A T C C C C N A N G C G N	- - - - -	- - - - -	49025 16S
750	A A A - G C G T G G G G A G C A A	- - - - -	- - - - -	- - - - -	49029 16S

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..... A C A G G A T T A G A T . C C C . . . G T A G T C C . . C . Consensus #1
 - - - - - A C A G G A T T A G A T A C C C T G - G T A G T C C - A C G Majority

810 820 830 840
 - - - - - A C A G G A T T A G A T A C C C T G - G T A G T C C - A C G 43030 16s
 769 G G G A A G C A A A C A G G A T T A G A T T C C C N T T G T A G T C C C G C C 49025 16s
 778 - - - - - A C A G G A T T A G A T A C C C T G - G T A G T C C - A C G 49029 16s
 766

C C G T A A . C . A T G A G T . C T . A G . T G T T G G G G G C A C C C Consensus #1
 C C G T A A A C G A T G A G T G C T - A G G T G T T G G G G G G A C A C A C C C Majority

850 860 870 880
 C C G T A A A C G A T G A G T G C T - A G G T G T T G G G G G G A C A C A C C C 43030 16s
 797 C C G T A A A C N A T G A G T A C T T A G T T G T T G G G G G A A C A C A C C C 49025 16s
 818 C C G T A A A C G A T G A G T G C T - A G G T G T T G G G G G G T A C C A C C C 49029 16s
 794

. C A . T G C . G . . G G A A A . C C A A T A A G C A C T C C G C C T G G G G A Consensus #1
 - C A G T G C C G A A G G A A A C C C A A T A A G C A C T C C G C C T G G G G A Majority

890 900 910 920
 - C A G T G C C G A A G G A A A M C C A A T A A G C A C T C C G C C T G G G G A 43030 16s
 836 - C A N T G C - G N G G A A A C C C A A T A A G C A C T C C G C C T G G G G A 49025 16s
 858 T C A G T G C C G A A G G A A A C C C A A T A A G C A C T C C G C C T G G G G A 49029 16s
 833

G T . C G G T C . C A A G A C T G A A . C T C A A A G G A A T T G A C G G G G G Consensus #1
 G T A C G G T C G C A A G A C T G A A A C T C A A A G G A A T T G A C G G G G G Majority

930 940 950 960
 G T A C G G T C G C A A G A C T G A A A C T C A A A G G A A T T G A C G G G G G 43030 16s
 875 G T G G T C N C A A G A C T G A A N C T C A A A G G A A T T G A C G G G G G 49025 16s
 896 G T A C G G T C G C A A G A C T G A A A C T C A A A G G A A T T G A C G G G G G 49029 16s
 873

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C C C G C A C A A G C A G T G G A G C A T . T G G T T T A A . T C G A A G C A A Consensus #1
C C C G C A C A A G C A G T G G A G C A T T T A A T T C G A A G C A A Majority

970 980 990 1000
C C C G C A C A A G C A G T G G A G C A T G T G G T T T A A A T C G A A G C A A 43030 16s
C C C G C A C A A G C A G T G G A G C A T N T G G T T T A A T T C G A A G C A A 49025 16s
C C C G C A C A A G C A G T G G A G C A T G T G G T T T A A T T C G A A G C A A 49029 16s

C G C G A A G A A C C T T A . C A G G G C T . G A C A T C C C . C T G A C . . Consensus #1
C G C G A A G A A C C T T A C C A G G G C T X G A C A T C C C T C T G A C A G C Majority

1010 1020 1030 1040
C G C G A A G A A C C T T A C C A G G G C T T G A C A T C C C T C T G A C A C C 43030 16s
C G C G A A G A A C C T T A C C A G G G C T T N G A C A T C C C T C T G A C C G G 49025 16s
C G C G A A G A A C C T T A N C A G G G C T C G A C A T C C C C C T G A C A G C 49029 16s

. . C A G A G A T G T C C C C T T C G G G G C A G . G G A G A C A G G T Consensus #1
C G C A G A G A T G X G G X T T C C C C T T C G G G G C A G A G G A C A G G T Majority

1050 1060 1070 1080
C T C A G A G A T G A G G G T C C C C T T C G G G G C A G A G G A C A G G T 43030 16s
T G C A G A G A T G T A C C T T C C C C T T C G G G G C A G A G G A C A G G T 49025 16s
C G C A G A G A T G C G G T T T C C C C T T C G G G G C A G G G A G A C A G G T 49029 16s

G G T G C A T G G T T G T C G T C A G C T C G T G T C G T G A G A T G T T G G G Consensus #1
G G T G C A T G G T T G T C G T C A G C T C G T G T C G T G A G A T G T T G G G Majority

1090 1100 1110 1120
G G T G C A T G G T T G T C G T C A G C T C G T G T C G T G A G A T G T T G G G 43030 16s
G G T G C A T G G T T G T C G T C A G C T C G T G T C G T G A G A T G T T G G G 49025 16s
G G T G C A T G G T T G T C G T C A G C T C G T G T C G T G A G A T G T T G G G 49029 16s

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TT . A G T C C C G C A A C G A G C G C C A C C C C T T G A . C T G T G T T A C C Consensus #1
 T T A A G T C C C G C A A C G A G C G C C A A C C C T T G A X C T G T G T T A C C Majority

	1130	1140	1150	1160	
1075	T T C A G T C C C G C A A C G A G C G C C A A C C C T T G A C	C T G T G T T A C C	43030 16s		
1096	T T A A G T C C C G C A A C G A G C G C C A A C C C T T G A C	T C T G T G T T A C C	49025 16s		
1073	T T A A G T C C C G C A A C G A G C G C C A A C C C T T G A C	A C T G T G T T A C C	49029 16s		

AGC . CGT . . . GG . GGGG A C T C A C A G . T G A C T G C C G G C C G T A Consensus #1
 AGC A C G T T G A G G T G G G G A C T C A C A G G T G A C T G C C G G C C G T A Majority

	1170	1180	1190	1200	
1115	A G C G C G T T G A G G C G G G G A C T C A C A G G T G A C T G C C G G C C G T A	43030 16s			
1136	A G C A C G T T G T G G T G G G G A C T C A C A G G T G A C T G C C G G C C G T A	49025 16s			
1113	A G C A C G T G A A G G T G G G G A C T C A C A G T T G A C T G C C G G C C G T A	49029 16s			

AGT C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C Consensus #1
 AGT C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C Majority

	1210	1220	1230	1240	
1155	A G T C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C	43030 16s			
1176	A G T C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C	49025 16s			
1153	A G T C G G A G G A A G G C G G G G A T G A C G T C A A A T C A T C A T G C C C	49029 16s			

. T . A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C C G G . A C Consensus #1
 T T T A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C C G T A C Majority

	1250	1260	1270	1280	
1195	C T G A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C C G G A C	43030 16s			
1216	T T T A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C C G G T A C	49025 16s			
1193	T T T A T G T C C T G G G C T A C A C A C G T G C T A C A A T G G G C C G G T A C	49029 16s			

Alignment 1

A A . G G G A . G C G A . . C C G C G A G G . G G A G C . A A . C C . . . A A A Consensus #1
A A C G G G A A G C G A A G C C G C G A G G T G G A G C C A A A C C C A A A A Majority

1235 A A A G G G A G C C G A A G C C G C G A G G C G G A G C G A A A C C C A A A A 43030 16s
1256 A A C G G G A A G C G A A G C C G C G A G G T G G A G C C A A A A A A 49025 16s
1233 A A C G G G A A G C G A A G A C C G C G A G G T G G A G C C A A A C C C T G A A A A 49029 16s

G C C G . T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A Consensus #1
G C C G T T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A Majority

1275 G C C G C T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A 43030 16s
1296 G C C G T T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A 49025 16s
1273 G C C G T T C G T A G T T C G G A T T G C A G G C T G C A A C T C G C C T G C A 49029 16s

T G A A G C C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C Consensus #1
T G A A G C C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C Majority

1315 T G A A G C C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C 43030 16s
1336 T G A A G C C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C 49025 16s
1313 T G A A G C C C G G A A T T G C T A G T A A T C G C G G A T C A G C A T G C C G C 49029 16s

G G T G A A T . C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C Consensus #1
G G T G A A T C C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C Majority

1355 G G T G A A T A C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C 43030 16s
1376 G G T G A A T C C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C 49025 16s
1353 G G T G A A T C C G T T C C C G G G C C T T G T A C A C A C C G C C C G T C A C 49029 16s

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A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G . G G T A A C C Consensus #1
A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G A G G T A A C C Majority

1450 1470 1480
1395 A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G A G G T A A C C 43030 16s
1416 A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G A G G T A A C C 49025 16s
1393 A C C A C G A G A G T C G G C A A C A C C C G A A G T C G G T G A G G T A A C C 49029 16s

. T G G A G C C A G C C G C C G A A G G T G G G G T . G A T G A T T G Consensus #1
C X T X T X G G G A G C C A G C C C G C C G A A G G T G G G G T T G A T G A T T G Majority

1490 1500 1510 1520
1435 C C T G T G G G A G C C C A G C C C G C C G A A G G T G G G G T C G A T G A T T G 43030 16s
1456 G T T A T - - G G A G C C C A G C C C G A A G G T G G G G T T G A T G A T T G 49025 16s
1433 C G T - C A G G G A G C C C A G C C C G C C G A A G G T G G G G T T G A T G A T T G 49029 16s

G G G T G A A G T C G T A A C A A G G T A G C C G T Consensus #1
G G G T G A A G T C G T A A C A A G G T A G C C G T Majority

1530 1540
1475 G G G T G A A G T C G T A A C A A G G T A G C C G T 43030 16s
1494 G G G T G A A G T C G T A A C A A G G T A G C C G T 49025 16s
1472 G G G T G A A G T C G T A A C A A G G T A G C C G T 49029 16s

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Figure 2

Sequence, 49029 16S
5 AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCCCTAATACATGCAAGTCGAGCGGACCCCTTCGGGGTCAGCGG
CGGACGGGTGAGTAACACGTGGGTAAATCTGCCCAAATGACCGGAATAACGCCTGGAAACGGGTGCTAAATGCCGATAGGC
AGCGAGCAGGCATCTGCTCGCTGGGAAAGGTGCAACCGCAGATGGAGGAGCCCGCGCGCATTAGCTGTTGGTG
GGGTAAACGGCTCACCAAGGCACGATGCGTAGCCGACCTGAGAGGTTGGACGGCCACACTGGGACTGAGACACCGGCCAG
ACTCCTACGGGAGGCAGTAGGGAATCTTCCGCCAATGGGCGCAAGCCTGACCGAGCAACGCCGCGTGAGCGGAAGG
CCTTCGGGTTGTAAAGCTCAGTCACCTCGGGAAGAGCGGCAAGGGAGTGGAAAGCCCTTGAGAGACGGTACCGAGAGAG
10 GAAGCCCCGGCTAACTACGTGCCAGACCGCGGGTAATACGTAGGGGCAAGCGTTGTCCGGAATCACTGGGCGTAAAGC
GTGCGTAGGCGGTTGCCGTGTCTCCGGGTGAAAGTCCAGGGCTCAACCCCTGGGAATGCCCTTGGAAACTGCGTAACTTGAG
TGCTGGAGAGCAAGGGAAATTCGCGGTGTAGCGGTGGAATGCGTAGATATGCGGAGGAATACCAAGTGCGCGAAGGCCCT
TGCTGGACAGTGACTGACGCTGAGGCACGAAGCGTGGGAGCAACACAGGATTAGATAACCCCTGCTAGTCCACGCCGTAA
CGATGAGTGTAGGTGTTGGGGGTACCAACCTCAGTGCCGAAGGAAACCCCAATAAGCACTCCGCCCTGGGGAGTACGGTC
15 GCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCCGACAAGCAGTGGAGCATGTGGTTTAAATTCGAAGCAACGCGAAGA
ACCTTANCAGGGCTCGACATCCCCCTGACAGCCGACAGATGCGGTTTCCCTTCGGGGCAGGGAGACAGGTGGTGCAATG
GTTGTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTTGAACGTGTGTACCAACGACGTCG
AAGGTGGGACTCACAGTTGACTGCCGGCGTAAGTCGGAGGAAGCGGGGATGACGTCAAATCATCATGCCCTTTATGTC
CTGGGTACACACGTGCTACAATGGGCGGTACAACGGGAAGCGAGACCCGCGAGGTGGAGCAAAACCCCTGAAAGCCGTTCCG
20 TAGTTCGGATTGACAGGCTGCAACTCGCCCTGCATGAAGCCGGAAATTGCTAGTAAATCGCGGATCAGCATGCCGCGGTGAATC
CGTTCGCCGGCCCTGTACACACCCCGCTCACACACGAGAGTCGGCAACACCCGAAAGTCGGTGGGTAACCCCGTCAGGG
AGCCAGCCCCGAAAGGTGGGTTGATGATTGGGGTGAAATCGTAAACAAGGTAGCCGT

Figure 3

49025 16S
5 GACGAACGCTGGCGGCGTGCCCTAATACATGCAAGTCGAGCGAGCCCTTCGGGGCTAGCGGGGACGGGTGAGTAACACGT 80
GGGCAATCCGCCCTTTCAGACTGGAAATAACACTCGGAAACGGGTGCTAATGCCGGATAATACACGGGTAGGCATCTACTTG 160
TGTTGAAAGATGCAACTGCATCGCTGAGAGAGGCCCGCGGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGC 240
GACGATGCGTAGCCGACCTGAGAGGGTGACCCGGCCACACTGGGACTGAGACACGGCCACAGACTCCTACGGGAGGCAGCAG 320
TAGGGAATCTTCCGCAATGGGCGCAAGCCCTGACGGAGCAACGCCCGGTGAGCGAAGAAAGCCCTTCGGGTTGTAAAGCTCT 400
GTTGCTCGGGGAGAGCGACAAAGGAGAGTGGAAGCTCCTTGTGAGACGGTACCGAGTGAGGAAGCCCCGGCTAACTACGT 480
GCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTGTCCGGAATCACTGGGCGGTAAAGCGTGCGTANGCGGTTGTGTA 560
AGTCTGAACTGAAAGTCCAAAGGCTCNACCTTGGGNATGCTTTGGAACCTGCATGGACTTGAGTGTCTGGAGAGGCNAGGCN 640
AATTCCNCGTGTACCGGTGNAATGCCGNTANATATGTGGAGGAATACCAAGTGGCNAANGCCCTTTGCTGGACAGTGGA 720
CTGACGCTGAAGGCACGAAANCGTGGGGANCAACNGGATTANATCCCNAAANGCGGGGAAGCAACAGGATTAGATT 800
CCCNTTGTAGTCCCGCCCGTAANCNATGAGTACTTAGTTGTTGGGGAACACACCCCAANTGCGNGGAAACCCCAATAAG 880
CACTCCGCCCTGGGAGTGGGTCNCAAGACTGAANCTCAAAGGAATTGACGGGGGCGCCGCAAGCAGTGGAGCATNTGG 960
TTTAAATTCGAAGCAACGGAAGAACCTTACCAGGGCTNGACATCCCTCTGACCCGGTGCAGAGATGTACCTTCCCTTCGGG 1040
GCAGAGGAGACAGGTGGTGCATGGTTGTCTCGTCAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCC 1120
TTGATCTGTGTTACCAGCACGTTGTGGTGGGACTCACAGGTGACTGCCGGCGTAAGTCGGAGGAAGCGGGGATGACGT 1200
CAAAATCATCATGCCCTTTATGTCTGGGCTACACACGTGCTACAATGGGCGGTACAACGGGAAGCGAGCCGCGAGGTGG 1280
AGCAAAACCTAAAAGCCGTTTCGTAGTTTCGGATTGCAGGCTGCAACTCGCCCTGCATGAAGCCGGAAATTGCTAGTAATCGC 1360
GGATCAGCATGCCGCGGTGAATCCGTTCCCGGGCCTTGTAACAACCGCCCGTCAACCAAGAGTCGGCAACACCCCGAA 1440
GTCGGTGAGGTAACCGTTATGGAGCCAGCCCGCGAAGGTGGGTTGATGATTGGGGTGAAGTCGTAACAAGGTAGCCGT 1519

Figure 4

43030 16S
 5 AGAGTTTGATCCTGGCTCAGGACGAACGGTGGCGGGTGCCTAATACATGCAAGTCGAGCGGGTCTCTTTCGGAGGCCAGC
 GCGGACGGGTGAGGAACACGTGGGTAACTTGCCCTTTCAGGCCGGAAATAACGCCCGGAAACGCGCGCTAAAGCCGGATAC
 GCCCGGAGGAGGCATCTTCTTTCGGGGAAGGCCCAATTGGGTGCTGAGAGAGGAGCCCCGCGGCATTAGCTAGTTG
 GCGGGTAACGGCCCAACCAAGGCACGATGCGTAGCCGACCTGAGAGGGTGACCGGCCACACTGGGACTGAGACACGCGC
 CAGACTCCTACGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGCAAGCCTGACGGAGCAACGCCGCGTGAGCGGAAGA
 AGGCCCTTCGGGTTGTAAAGCTCTGTTGCTCGGGGAGAGCGGCATGGGGATGGAAGCCCGTGCGAGACGGTACCGAGT
 GAGGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAAACGTAGGGGCGAGCGTGTGTCCGGAATCAC'TGGGCGTAA
 AGGTGCGTAGGCCGTGAGCAAGTCTGGAGTGAAAGTCCATGGCTCAACCATGGGATGGCTTTGGAAACTGCTTGACTT
 GAGTGTGGAGAGCAAGGGGAATTCCACGTGTAGCGGTGAAATGCGTAGAGATGTGGAGGAATACCAAGTGGCGAARGCG
 CCTTGCTGGACAGTGACTGACGCTGAGGCACGAAGCGTGGGGAGCAAAACAGGATTAGATACCCCTGGGAGTCCACGCCGT
 AAACGATGAGTGCTAGGTGTTGGGGGACACACCCCAAGTCCCGAAGGAAAMCCAATAAGCACTCCGCTGGGAGTACGG
 TCGCAAGACTGAACCTCAAAGGAATTGACGGGGCCCCGACAAAGCAGTGGAGCATGTGGTTTAAATCGAAGCAACGCCGA
 GAACCTTACCAGGGCTTGACATCCCTCTGACACCCCTCAGAGATGAGGGTCCCTTCGGGGCAGAGGACAGGTGGTGCA
 TGGTTGTCGTCAAGTTCGTGAGATGTTGGGTTCAGTCCCGCAACGAGCGCAACCCCTTGACCTGTGTACCAGCGCG
 TTGAGCGGGGACTCACAGGTGACTGCCGGCGTAAGTCGGAGGAAGCGGGGATGACGTCAAATCATCATGCCCTGATG
 TCCTGGGCTACACACGTGCTACAAATGGGCGGAACAAAGGAGGCGGAAGCCGCGAGGCGGAGCGAAACCCAAAAGCCGCT
 CGTAGTTCGGATTGCAGGCTGCAACTCGCCTGCAATGAAGCCGGAATTGCTAGTAATCGCGGATCAGCATGCCCGCGTGAA
 TACGTTCCCGGCCCTTGTAACACACCGCCCGTCACACCACGAGAGTCGGCAACACCCGAAGTCGGTGAGGTAAACCCCTGTG
 GGGAGCCAGCCCGCGAAGGTGGGTCGATGATTGGGTGAAGTCGTAAACAAGGTAGCCGT

Figure 5: Shc polynucleotide sequence alignments

Cloned ac 43030: Cloned *Alicyclobacillus acidocaldarius* ATCC43030
 Cloned at 43030: Cloned *Alicyclobacillus acidoterrestris* ATCC49025
 Blast ac: sequence of *A. acidocaldarius* got from the blast database
 Blast at: sequence of *A. acidocaldarius* got from the blast database

Primer and probe ranges were highlighted red

```

10      G G G G G T T G G A T G T T C C A G G C Majority
      -----+-----
              10                      20
      -----+-----

15      1 G G G G G T T G G A T G T T A C A G G C cloned ac 43030 shc
      1 G G A G G A T G G A T G T T T C A G G C Blast ac shc
      1 G G A G G G T G G A T G T T C C A G G C cloned at 49025 shc
      1 G G G G G T T G G A T G T T C C A G G C Blast at shc

20      T T G T A T T T C T C C A G T G T G G G Majority
      -----+-----
              30                      40
      -----+-----

25      21 T T C C A T C T C G C C C G T G T G G G cloned ac 43030 shc
      21 T T C C A T C T C G C C G G T G T G G G Blast ac shc
      21 G A G T A T T T C T C C A A T C T G G G cloned at 49025 shc
      21 G A G T A T T T C T C C A A T C T G G G Blast at shc

30      A T A C T G G C T T G G C C G T G T T G Majority
      -----+-----
              50                      60
      -----+-----

35      41 A C A C G G G T C T C G C C G T G C T C cloned ac 43030 shc
      41 A C A C G G G C C T C G C C G T G C T C Blast ac shc
      41 A T A C T G G C T T G A C C G T C T T G cloned at 49025 shc
      41 A T A C T G G C T T G A C C G T C T T G Blast at shc

40      G C G C T G C G T T C T G C T G G G T T Majority
      -----+-----
              70                      80
      -----+-----

45      61 G C G C T G C G C G C T G C G G G G C T cloned ac 43030 shc
      61 G C G C T G C G C G C T G C G G G G C T Blast ac shc
      61 G C A C T G C G T T C G G C T G G A T T cloned at 49025 shc
      61 G C A C T G C G T T C G G C T G G A T T Blast at shc

50      T C C G G C C G A T C A T - G C C G G G Majority
      -----+-----
              90                      100
      -----+-----

55      81 T C C G G C C G A T C A C T G A C C G G cloned ac 43030 shc
      81 T C C G G C C G A T C A C - G A C C G C Blast ac shc
      81 G C C A C C A G A T C A T - C C A G C G cloned at 49025 shc
      81 G C C A C C A G A T C A T - C C A G C G Blast at shc
    
```

Figure 5: Shc polynucleotide sequence alignments (continued)

		T T G G T T A A G G C - - G G G T G A G Majority											
5		-----+-----+-											
		110						120					
		-----+-----+-											
	101	T T G G T C A A G G C T G G G C T G A A cloned ac 43030 shc											
	100	T T G G T C A A G G C - - G G G C G A G Blast ac shc											
10	100	C T G A T T A A A G C - - G G G T G A G cloned at 49025 shc											
	100	C T G A T T A A A G C - - G G G T G A G Blast at shc											
		T G G T T G T T G G G T C G G C A G A T Majority											
		-----+-----+-											
15		130						140					
		-----+-----+-											
	121	T G G C T G T T G G A C C G G C A G A T cloned ac 43030 shc											
	118	T G G C T G T T G G A C C G G C A G A T Blast ac shc											
	118	T G G T T G G T C A G T A A A C A A A T cloned at 49025 shc											
20	118	T G G T T G G T C A G T A A A C A A A T Blast at shc											
		T C T C G T G G C T G G C G A C T G G G Majority											
		-----+-----+-											
		150						160					
		-----+-----+-											
25	141	C A C C G T G C C G G G C G A T T G G G cloned ac 43030 shc											
	138	C A C G G T T C C G G G C G A C T G G G Blast ac shc											
	138	T C T C A A G G A T G G C G A C T G G A cloned at 49025 shc											
	138	T C T C A A G G A T G G C G A C T G G A Blast at shc											
30		A G G T T C G T C G C C G G A A G G T G Majority											
		-----+-----+-											
		170						180					
		-----+-----+-											
35	161	T G G T G A A G C G C C C G A A C C T C cloned ac 43030 shc											
	158	C G G T G A A G C G C C C G A A C C T C Blast ac shc											
	158	A A G T T C G T C G A C G C A A G G C G cloned at 49025 shc											
	158	A A G T T C G T C G A C G C A A G G C G Blast at shc											
40		A A A C C G G G C G G T T T G G C G T T Majority											
		-----+-----+-											
		190						200					
		-----+-----+-											
45	181	A A C C C G G G C G G C T T C G C G C T cloned ac 43030 shc											
	178	A A G C C G G G C G G G T T C G C G T T Blast ac shc											
	178	A A A C C A G G C G G T T G G G C A T T cloned at 49025 shc											
	178	A A A C C A G G C G G T T G G G C A T T Blast at shc											
		T G A G T T C G A C T G C G T G T A C T Majority											
		-----+-----+-											
50		210						220					
		-----+-----+-											
	201	C C A G T T C G A C A A A C G T G T A C T cloned ac 43030 shc											
	198	C C A G T T C G A C A A A C G T G T A C T Blast ac shc											
55	198	T G A A T T C C A C T G C G A A A A C T cloned at 49025 shc											
	198	T G A A T T C C A C T G C G A A A A C T Blast at shc											

Figure 5: Shc polynucleotide sequence alignments (continued)

		A C C C G G A C G T G G A C G A T A C G	Majority
		-----+-----+-----	
5		230 240	
		-----+-----+-----	
	221	A T C C G G A C G T G G A C G A C A C G	cloned ac 43030 shc
	218	A C C C G G A C G T G G A C G A C A C G	Blast ac shc
	218	A C C C A G A C G T C G A C G A T A C G	cloned at 49025 shc
10	218	A C C C A G A C G T C G A C G A T A C G	Blast at shc
		G C G G T G G T C G T C T T G G C G C T	Majority
		-----+-----+-----	
		250 260	
		-----+-----+-----	
15	241	G C C G T C G T C A T C T G G G C G C T	cloned ac 43030 shc
	238	G C C G T C G T G G T G T G G G C G C T	Blast ac shc
	238	G C G A T G G T C G T C T T G G C G C T	cloned at 49025 shc
	238	G C G A T G G T C G T C T T G G C G C T	Blast at shc
20		C A A T G G C C T T C G A T T G C C G G	Majority
		-----+-----+-----	
		270 280	
		-----+-----+-----	
25	261	C A A C A C G C T G C G A C T C C C G G	cloned ac 43030 shc
	258	C A A C A C C C T G C G C T T G C C G G	Blast ac shc
	258	C A A T G G C A T T C A A T T G C C G G	cloned at 49025 shc
	258	C A A T G G C A T T C A A T T G C C G G	Blast at shc
30		A T G A G G G G C G G C G T C G T G A C	Majority
		-----+-----+-----	
		290 300	
		-----+-----+-----	
35	281	A C G A G C G C C G C A G G C G A G A C	cloned ac 43030 shc
	278	A C G A G C G C C G C A G G C G G G A C	Blast ac shc
	278	A T G A A G G G A A G C G T C G T G A C	cloned at 49025 shc
	278	A T G A A G G G A A G C G T C G T G A C	Blast at shc
		G C C T T G A C G C G T G G C T T C C G	Majority
		-----+-----+-----	
40		310 320	
		-----+-----+-----	
	301	G C C A T G A C G A A G G G A T T C C G	cloned ac 43030 shc
	298	G C C A T G A C G A A G G G A T T C C G	Blast ac shc
45	298	G C A T T G A C C C G T G G C T T C C G	cloned at 49025 shc
	298	G C A T T G A C C C G T G G C T T C C G	Blast at shc
		T T G G T T T G T C G G G A T G C A G A	Majority
		-----+-----+-----	
50		330 340	
		-----+-----+-----	
	321	C T G G A T T G T C G G C A T G C A G A	cloned ac 43030 shc
	318	C T G G A T T G T C G G C A T G C A G A	Blast ac shc
	318	T T G G T T G C G C G A G A T G C A G A	cloned at 49025 shc
55	318	T T G G T T G C G C G A G A T G C A G A	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		G T T C G A A C G G G G G C T G G G G C	Majority
		-----+-----+-----	
5		350 360	
		-----+-----+-----	
	341	G C T C G A A C G G C G G C T G G G G C	cloned ac 43030 shc
	338	G C T C G A A C G G C G G T T G G G G C	Blast ac shc
	338	G T T C G A A C G G G G G C T G G G G C	cloned at 49025 shc
10	338	G T T C G A A C G G G G G C T G G G G C	Blast at shc
		G C A T A C G A T G T G G A C A A C A C	Majority
		-----+-----+-----	
		370 380	
		-----+-----+-----	
15	361	G C A T A C G A C G T C G A C A A C A C	cloned ac 43030 shc
	358	G C C T A C G A C G T C G A C A A C A C	Blast ac shc
	358	G C A T A C G A T G T G G A C A A C A C	cloned at 49025 shc
	358	G C A T A C G A T G T G G A C A A C A C	Blast at shc
20		G C G T G A T T T G C C G A A - T C G G	Majority
		-----+-----+-----	
		390 400	
		-----+-----+-----	
25	381	G A G C G A T C T C C C G A A - C C A C	cloned ac 43030 shc
	378	G A G C G A T C T C C C G A A - C C A C	Blast ac shc
	378	G C G T C A G T T G A C C A A - T C G G	cloned at 49025 shc
	378	G C G T C A G T T G A C C A A A T C G G	Blast at shc
30		A T T C C G T T T T - G C G A C T T C G	Majority
		-----+-----+-----	
		410 420	
		-----+-----+-----	
35	400	A T C C C G T T C T - G C G A C T T C G	cloned ac 43030 shc
	397	A T C C C G T T C T - G C G A C T T C G	Blast ac shc
	397	A T T C C A T T T T - G C A A C T T C G	cloned at 49025 shc
	398	A T T C C A T T T T T G C G A C T T C G	Blast at shc
40		G - C G A A G T G A T T G A T C C G C C	Majority
		-----+-----+-----	
		430 440	
		-----+-----+-----	
45	419	G - C G A A G T G A C C G A T C C G C C	cloned ac 43030 shc
	416	G - C G A A G T G A C C G A T C C G C C	Blast ac shc
	416	G - C G A A G T G A T T G A T C C G C C	cloned at 49025 shc
	418	G G C G A A G T G A T T G A T C C G C C	Blast at shc
50		G T C G G A A G A C G T C A C C G C C C	Majority
		-----+-----+-----	
		450 460	
		-----+-----+-----	
	438	G T C G G A A G A C G T C A C C G C C C	cloned ac 43030 shc
	435	G T C A G A G G A C G T C A C C G C C C	Blast ac shc
	435	A T C G G A A G A C G T C A C C G C C A C	cloned at 49025 shc
55	438	A T C G G A A G A C G T C A C C G C C A C	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		A C G T G T T G G A G T G T T T C G G C	Majority
		-----+-----+-----	
5		470 480	
		-----+-----+-----	
	458	A C G T G C T C <u>G A G T G T T T C G G C</u>	cloned ac 43030 shc
	455	A C G T G C T C <u>G A G T G T T T C G G C</u>	Blast ac shc
	455	A C G T C T T G <u>G A G T G C T T C G G C</u>	cloned at 49025 shc
10	458	A C G T C T T G <u>G A G T G C T T C G G C</u>	Blast at shc
		A G C T T T G G G T A C G A C G A G G C	Majority
		-----+-----+-----	
		490 500	
		-----+-----+-----	
15	478	<u>A G C T T</u> C G G C T A C G A C G A C G C	cloned ac 43030 shc
	475	<u>A G C T T</u> C G G G T A C G A T G A C G C	Blast ac shc
	475	<u>A G C T T</u> T G G G T A C G A C G A G G C	cloned at 49025 shc
	478	<u>A G C T T</u> T G G G T A C G A C G A G G C	Blast at shc
20		C T G G A A G G T G A T T C G G C G G G	Majority
		-----+-----+-----	
		510 520	
		-----+-----+-----	
25	498	C T G G A A G G T G A T C C A G C G C G	cloned ac 43030 shc
	495	C T G G A A G G T C A T C C G G C G C G	Blast ac shc
	495	A T G G A A G G T G A T T C G C A A G G	cloned at 49025 shc
	498	A T G G A A G G T G A T T C G C A A G G	Blast at shc
30		C G G T G G A G T A T C T C A A G G G G	Majority
		-----+-----+-----	
		530 540	
		-----+-----+-----	
35	518	C G G T G G C G T A C C T C A A G C G G	cloned ac 43030 shc
	515	C G G T G G A A T A T C T C A A G C G G	Blast ac shc
	515	C G G T C G A G T A T C T C A A G G C G	cloned at 49025 shc
	518	C G G T C G A G T A T C T C A A G G C G	Blast at shc
40		G A G C A G C G G C C G G A T G G G T G	Majority
		-----+-----+-----	
		550 560	
		-----+-----+-----	
45	538	G A G C A G A A G C C G G A C G G C A G	cloned ac 43030 shc
	535	G A G C A G A A G C C G G A C G G C A G	Blast ac shc
	535	C A A C A A C G C C C A G A T G G G T C	cloned at 49025 shc
	538	C A A C A A C G C C C A G A T G G G T C	Blast at shc
50		C T G G T T T G G T C G C T G G G G C G	Majority
		-----+-----+-----	
		570 580	
		-----+-----+-----	
55	558	C T G G T T C G G T C G C T G G G G C G	cloned ac 43030 shc
	555	C T G G T T C G G T C G T T G G G G C G	Blast ac shc
	555	A T G G T T T G G C C G C T G G G G C G	cloned at 49025 shc
	558	A T G G T T T G G C C G C T G G G G C G	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		T C A A C T A C G T G T A T G G C A T G	Majority
		-----+-----	
5		590 600	
		-----+-----	
	578	T C A A C T A C A T C T A C G G C A C G	cloned ac 43030 shc
	575	T C A A T T A C C T C T A C G G C A C G	Blast ac shc
	575	T C A A C T A C G T G T A T G G C A T C	cloned at 49025 shc
10	578	T C A A C T A C G T G T A T G G C A T C	Blast at shc
		G G C G C G G T G G T T T C G G G G C T	Majority
		-----+-----	
		610 620	
		-----+-----	
15	598	G G C G C G G T G G T G T C G G C G C T	cloned ac 43030 shc
	595	G G C G C G G T G G T G T C G G C G C T	Blast ac shc
	595	G G C G C G G T C G T T C C G G G A C T	cloned at 49025 shc
	598	G G C G C G G T C G T T C C G G G A C T	Blast at shc
20		G A A G G C G G T C G G T G T C G A T A	Majority
		-----+-----	
		630 640	
		-----+-----	
25	618	G A A G G C G G T C G G G A T C G A C A	cloned ac 43030 shc
	615	G A A G G C G G T C G G G A T C G A C A	Blast ac shc
	615	C A A G G C C G T C G G T G T C G A T A	cloned at 49025 shc
	618	C A A G G C C G T C G G T G T C G A T A	Blast at shc
30		T G C G T G A G C C G T G G G T T C A A	Majority
		-----+-----	
		650 660	
		-----+-----	
35	638	T G C G C G A G C C G T A C A T T C A A	cloned ac 43030 shc
	635	C G C G C G A G C C G T A C A T T C A A	Blast ac shc
	635	T G C G T G A G C C G T G G G T G C A A	cloned at 49025 shc
	638	T G C G T G A G C C G T G G G T G C A A	Blast at shc
40		A A G T C G C T C G A C T G G G T C G T	Majority
		-----+-----	
		670 680	
		-----+-----	
45	658	A A G G C G C T C G A T T G G G T G G A	cloned ac 43030 shc
	655	A A G G C G C T C G A C T G G G T C G A	Blast ac shc
	655	A A G T C G C T C G A C T G G C T C G T	cloned at 49025 shc
	658	A A G T C G C T C G A C T G G C T C G T	Blast at shc
50		G G A G C A T C A G A A T G C G G A T G	Majority
		-----+-----	
		690 700	
		-----+-----	
	678	G C A G C A T C A G A A C C C G G A C G	cloned ac 43030 shc
	675	G C A G C A T C A G A A C C C G G A C G	Blast ac shc
	675	C G A G C A T C A A A A T G A G G A T G	cloned at 49025 shc
55	678	C G A G C A T C A A A A T G A G G A T G	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		G C G G C T G G G G T G A A G A C T G - Majority	
		-----+-----	
5		710 720	
		-----+-----	
	698	G	cloned ac 43030 shc
	695	G C G G C T G G G G C G A G G A C T G -	Blast ac shc
	695	G C G G C T G G G G T G A A A G C C G A	cloned at 49025 shc
10	698	G C G G T T G G G G T G A A G A T T G -	Blast at shc
		- - C C G X T C X T A C G A G G A T C C Majority	
		-----+-----	
		730 740	
		-----+-----	
15	698		cloned ac 43030 shc
	714	- - C C G C T C G T A C G A G G A T C C	Blast ac shc
	715	A T T C C A G C A C A C T G G C G G C C	cloned at 49025 shc
	717	- - C C G T T C C T A T G A T G A T C C	Blast at shc
20		G X X X C T C G C G G G T C A G G G C G Majority	
		-----+-----	
		750 760	
		-----+-----	
25	698		cloned ac 43030 shc
	732	G G C G T A C G C G G G T A A G G G C G	Blast ac shc
	735	G T T A C T A G T G G A T C C G A G C T	cloned at 49025 shc
	735	A C G T C T C G C A G G T C A G G G T G	Blast at shc
30		C G A G X A C A C C G T C G C A G A C X Majority	
		-----+-----	
		770 780	
		-----+-----	
35	698		cloned ac 43030 shc
	752	C G A G C A C C C C G T C G C A G A C G	Blast ac shc
	755	C G G T A C C A A G C T T T G G C G T A A	cloned at 49025 shc
	755	T G A G T A C A C C G T C G C A G A C C	Blast at shc
40		G C C T G G G C G T T G A T G G C G C T Majority	
		-----+-----	
		790 800	
		-----+-----	
45	698		cloned ac 43030 shc
	772	G C C T G G G C G C T G A T G G C G C T	Blast ac shc
	775	T C A T G G T C A T A G C T G T T T C C	cloned at 49025 shc
	775	G C C T G G G C G T T G A T G G C G C T	Blast at shc
50		C A T C G C G G G C G G C X G T G T C G Majority	
		-----+-----	
		810 820	
		-----+-----	
	698		cloned ac 43030 shc
	792	C A T C G C G G G C G G C A G G G C G G	Blast ac shc
	795	T G T G T G A A A T T G - - G T A T C C	cloned at 49025 shc
55	795	C A T C G C G G G C G G C C G T G T C G	Blast at shc

Figure 5: Shc polynucleotide sequence alignments (continued)

		A G T C A G A X G C C G C A C X X C G C	Majority
		-----+-----	
5		830 840	
		-----+-----	
	698		cloned ac 43030 shc
	812	A G T C C G A G G C C G C G C G C C G C	Blast ac shc
	813	G C T C A C A A T T C A C A C A A C A T	cloned at 49025 shc
10	815	A G T C A G A T G C G G T A T T G C G C	Blast at shc
		G G G G T C C X X T A C C T X X X X G -	Majority
		-----+-----	
		850 860	
		-----+-----	
15	698		cloned ac 43030 shc
	832	G G C G T G C A A T A C C T C G T G G -	Blast ac shc
	833	A C G A G C C G G A A C A T A A G T G T	cloned at 49025 shc
	835	G G G G T C A C T T A C C T T C A C G -	Blast at shc
20		A X A C G C A G C G C G C X G A T G - G	Majority
		-----+-----	
		870 880	
		-----+-----	
25	698		cloned ac 43030 shc
	851	A G A C G C A G C G C C C G G A C G - G	Blast ac shc
	853	A A G C C T G G G G T G C C T A T G A G	cloned at 49025 shc
	854	A C A C G C A G C G C C A G A T G - G	Blast at shc
30		T G G C T G X X X	Majority

35	698		cloned ac 43030 shc
	870	C G G C T G G G A	Blast ac shc
	873	T G A G C T	cloned at 49025 shc
	873	T G G C T G	Blast at shc

Figure 6: Shc amino acid sequence alignments

The degenerate primer range is highlighted red.

5		M T - - - - - E Q L V E A - Majority
		-----+-----
		10 20
		-----+-----
10	1	M A - - - - - E Q L V E A - A. acidocaldarius ATCC27009
	1	M A - - - - - E Q L V E A - A. acidocaldarius JCM 5260T
	1	M T - - - - - K Q L L D T - A. acidoterrestris DSM 3902
	1	M G T - - - - - Bacillus subtilis
	1	F T R M T T T N W S L K V D R G R Q T W Dictyostelium discoideum
	1	M V I A A S - - - - - Synechocystis sp. PCC 6803
15	1	M T A T T D G S T G A S L R P L A A S - Streptomyces coelicolor A3
		- - - - - P - - - - - Majority
		-----+-----
		30 40
		-----+-----
20	9	- - - - - P - - - - - A. acidocaldarius ATCC27009
	9	- - - - - P - - - - - A. acidocaldarius JCM 5260T
	9	- - - - - P - - - - - A. acidoterrestris DSM 3902
	4	- - - - - Bacillus subtilis
25	21	E Y S Q E K K E A T D V D I H L L R L K Dictyostelium discoideum
	7	- - - - - Synechocystis sp. PCC 6803
	20	- - - - - A S D T D I T I - - - - Streptomyces coelicolor A3
		- - - - - E A V A R Majority
		-----+-----
		50 60
		-----+-----
35	10	- - - - - A Y A R A. acidocaldarius ATCC27009
	10	- - - - - A Y A R A. acidocaldarius JCM 5260T
	10	- - - - - M V Q A A. acidoterrestris DSM 3902
	4	- - - - - L - - - - - Q E K V R R Bacillus subtilis
	41	E P G T H C P E G C D L N R A K T P Q Q Dictyostelium discoideum
	7	- P S V P C P S - - - - - T E Q V R Q Synechocystis sp. PCC 6803
	28	- P A A A A G V - - - - - P E A A A R Streptomyces coelicolor A3
40		A L D R A V D Y L L S R Q K A D G Y W W Majority
		-----+-----
		70 80
		-----+-----
45	14	T L D R A V E Y L L S C Q K D E G Y W W A. acidocaldarius ATCC27009
	14	T L D R A V E Y L L S C Q K D E G Y W W A. acidocaldarius JCM 5260T
	14	T L E A G V A H L L R R Q A P D G Y W W A. acidoterrestris DSM 3902
	11	F Q K K T I T E L R D R Q N A D G S W T Bacillus subtilis
	61	A I K K A F Q Y F S K V Q T E D G H W A Dictyostelium discoideum
50	20	A I A A S R D F L L S E Q Y A D G Y W W Synechocystis sp. PCC 6803
	41	A T R R A T D F L L A K Q D A E G W W K Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		G P L L S N V T M E A E Y V L L C H I L	Majority
		-----+-----+-----	
5		90 100	
		-----+-----+-----	
	34	G P L L S N V T M E A E Y V L L C H I L	A. acidocaldarius ATCC27009
	34	G P L L S N V T M E A E Y V L L C H I L	A. acidocaldarius JCM 5260T
	34	A P L L S N V C M E A E Y V L L C H C L	A. acidoterrestris DSM 3902
10	31	F C F E G P I M T N S F F I L L L T S L	Bacillus subtilis
	81	G D Y G G P M F L L P G L V I T C Y V T	Dictyostelium discoideum
	40	S E L E S N V T I T A E V V I L H K I W	Synechocystis sp. PCC 6803
	61	G D L E T N V T M D A E D L L L R Q F L	Streptomyces coelicolor A3
15		G R V D R E R - - M E K I R R Y L L H E	Majority
		-----+-----+-----	
		110 120	
		-----+-----+-----	
	54	D R V D R D R - - M E K I R R Y L L H E	A. acidocaldarius ATCC27009
20	54	D R V D R D R - - M E K I R R Y L L H E	A. acidocaldarius JCM 5260T
	54	G K K N P E R - - E A Q I R K Y I I S Q	A. acidoterrestris DSM 3902
	51	D E G E N E K E L I S S L A A G I H A K	Bacillus subtilis
	101	G Y Q L P E S T Q R E I I R Y L F N R Q	Dictyostelium discoideum
	60	G T A A Q R P - - L E K A K N Y L L Q Q	Synechocystis sp. PCC 6803
25	81	G I Q D E E T - - T R A A A L F I R G E	Streptomyces coelicolor A3
		Q R E D G T W A L Y P G G P - G D L S T	Majority
		-----+-----+-----	
		130 140	
		-----+-----+-----	
30	72	Q R E D G T W A L Y P G G P - P D L D T	A. acidocaldarius ATCC27009
	72	Q R E D G T W A L Y P G G P - P D L D T	A. acidocaldarius JCM 5260T
	72	R R E D G T W S I Y P G G P - S D L N A	A. acidoterrestris DSM 3902
	71	Q Q P D G T F I N Y P D E T R G N L T A	Bacillus subtilis
35	121	N P V D G G W G L H I E A H S D I F G T	Dictyostelium discoideum
	78	Q R D H G G W E L Y Y G D G - G E L S T	Synechocystis sp. PCC 6803
	99	Q R E D G T W A T F Y G G P - G E L S T	Streptomyces coelicolor A3
40		T V E A Y V A L K Y L G - V S A D E P H	Majority
		-----+-----+-----	
		150 160	
		-----+-----+-----	
	91	T I E A Y V A L K Y I G - M S R D E E P	A. acidocaldarius ATCC27009
	91	T I E A Y V A L K Y I G - M S R D E E P	A. acidocaldarius JCM 5260T
45	91	T V E A Y V A L K Y L G - E P A S D P Q	A. acidoterrestris DSM 3902
	91	T V Q G Y V G M L A S G C F H R T E P H	Bacillus subtilis
	141	T L Q - Y V S L R L L G - V P A D H P S	Dictyostelium discoideum
	97	S V E A Y T A L R I L G - V P A T D P A	Synechocystis sp. PCC 6803
	118	T I E A Y V A L R L A G - D S P E A P H	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		M V K A L E F I Q S Q G G I E S S R V F	Majority
		-----+-----	
5		170 180	
		-----+-----	
	110	M Q K A L R F I Q S Q G G I E S S R V F	A. acidocaldarius ATCC27009
	110	M Q K A L R F I Q S Q G G I E S S R V F	A. acidocaldarius JCM 5260T
	110	M V Q A K E F I Q N E G G I E S T R V F	A.acidoterrestris DSM 3902
10	111	M K K A E Q F I I S H G G L R H V H F M	Bacillus subtilis
	159	V V K A R T F L L Q N G G A T G I P S W	Dictyostelium discoideum
	116	L V K A K N F I V G R G G I S K S R I F	Synechocystis sp. PCC 6803
	137	M A R A A E W I R S R G G I A S A R V F	Streptomyces coelicolor A3
15		T R M W L A L V G E Y P W D K L P M I P	Majority
		-----+-----	
		190 200	
		-----+-----	
	130	T R M W L A L V G E Y P W E K V P M V P	A. acidocaldarius ATCC27009
20	130	T R M W L A L V G E Y P W E K V P M V P	A. acidocaldarius JCM 5260T
	130	T R L W L A M V G Q Y P W D K L P V I P	A.acidoterrestris DSM 3902
	131	T K W M L A A N G L Y P W P A L - Y L P	Bacillus subtilis
	179	G K F W L A T L N A Y D W N G L N P I P	Dictyostelium discoideum
	136	T K M H L A L I G C Y D W R G T P S I P	Synechocystis sp. PCC 6803
25	157	T R I W L A L F G W W K W D D L P E L P	Streptomyces coelicolor A3
		P E I M L L P K N V P L N I Y E F G S W	Majority
		-----+-----	
		210 220	
		-----+-----	
30	150	P E I M F L G K R M P L N I Y E F G S W	A. acidocaldarius ATCC27009
	150	P E I M F L G K R M P L N I Y E F G S W	A. acidocaldarius JCM 5260T
	150	P E I M H L P K S V P L N I Y D F A S W	A.acidoterrestris DSM 3902
	150	L S L M A L P P T L P I H F Y Q F S S Y	Bacillus subtilis
35	199	I E F W L L P Y N L P I A P G R W W C H	Dictyostelium discoideum
	156	P W V M L L P N N F F F N I Y E M S S W	Synechocystis sp. PCC 6803
	177	P E L I Y F P T W V P L N I Y D F G C W	Streptomyces coelicolor A3
40		A R A T V V P L S I V M A Q Q P V - - -	Majority
		-----+-----	
		230 240	
		-----+-----	
	170	A R A T V V A L S I V M S R Q P V - - -	A. acidocaldarius ATCC27009
	170	A R A T V V A L S I V M S R Q P V - - -	A. acidocaldarius JCM 5260T
45	170	A R A T I V T L S Y R H E S P T C - - -	A.acidoterrestris DSM 3902
	170	A R I H F A P M A V T L N Q R - - - -	Bacillus subtilis
	219	C R M V Y L P M S Y I Y A K K T T G P L	Dictyostelium discoideum
	176	A R S S T V P L M I V C D Q K P V - - -	Synechocystis sp. PCC 6803
	197	A R Q T I V P L T I V S A K R P V R P A	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		- F P L P E L A R V P E L Y E T D V P P	Majority
		-----+-----+	
5		250 260	
		-----+-----+	
	187	- F P L P E R A R V P E L Y E T D V P P	A. acidocaldarius ATCC27009
	187	- F P L P E R A R V P E L Y E T D V P P	A. acidocaldarius JCM 5260T
	187	- D A T S G L C K G S G I V R G E G P P	A.acidoterrestris DSM 3902
10	185	- F V L I N R - N I S S L H H L D - - P	Bacillus subtilis
	239	T D L V K D L R R - - E I Y C Q E Y E K	Dictyostelium discoideum
	193	- Y D I A Q G L R V D E L Y A E G M E N	Synechocystis sp. PCC 6803
	217	P F P L D E L H T D P A - - - R P N P P	Streptomyces coelicolor A3
15		R R - R G A K G G G G W - - - I F D A -	Majority
		-----+-----+	
		270 280	
		-----+-----+	
	206	R R - R G A K G G G G W - - - I F D A -	A. acidocaldarius ATCC27009
20	206	R R - R G A K G G G G W - - - I F D A -	A. acidocaldarius JCM 5260T
	206	K R - R S A K G G D S G - - - F F V A -	A.acidoterrestris DSM 3902
	201	H M T K N P F T W L R S - - D A F E E R	Bacillus subtilis
	257	I N W S E Q R N N I S K L D M Y Y E H T	Dictyostelium discoideum
	212	V Q Y K L P E S G T I W - - D I F I G -	Synechocystis sp. PCC 6803
25	234	R P - L A P V A S W D G - - - A F Q R -	Streptomyces coelicolor A3
		- L D S A L H G Y Q K A - - A V H P F R	Majority
		-----+-----+	
		290 300	
		-----+-----+	
30	221	- L D R A L H G Y Q K L - - S V H P F R	A. acidocaldarius ATCC27009
	221	- L D R A L H G Y Q K L - - S V H P F R	A. acidocaldarius JCM 5260T
	221	- L D K F L K A Y N K W - - P I Q P G R	A.acidoterrestris DSM 3902
	219	D L T S I L L H W K R V F H A P F A F Q	Bacillus subtilis
35	277	S L L N V I N G S L N A Y E K V H S K W	Dictyostelium discoideum
	229	- L D S L F K L Q E Q A - - K V V P F R	Synechocystis sp. PCC 6803
	249	- I D K A L H A Y R K V - - A P R R L R	Streptomyces coelicolor A3
40		R A G E A R A L T W I L E R Q E G D G S	Majority
		-----+-----+	
		310 320	
		-----+-----+	
	238	R A A E I R A L D W L L E R Q A G D G S	A. acidocaldarius ATCC27009
	238	R A A E I R A L D W L L E R Q A G D G S	A. acidocaldarius JCM 5260T
45	238	K S G E Q K A L E W I L A H Q E A D G C	A.acidoterrestris DSM 3902
	239	Q L G L Q T A K T Y M L D R I E K D G T	Bacillus subtilis
	297	L R D K A I D Y T F D H I R Y E D E Q T	Dictyostelium discoideum
	246	E Q G L A L A E K W I L E R Q E V S G D	Synechocystis sp. PCC 6803
	266	R A A M N S A A R W I I E R Q E N D G C	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		W G G I Q P P W F Y A L I A L K V L G M	Majority
		-----+-----	
5		330 340	
		-----+-----	
	258	W G G I Q P P W F Y A L I A L K I L D M	A. acidocaldarius ATCC27009
	258	W G G I Q P P W F Y A L I A L K I L D M	A. acidocaldarius JCM 5260T
	258	W G G I Q P P W F Y A L L A L K C L N M	A. acidoterrestris DSM 3902
10	259	L Y S Y A S A T I Y M V Y S L L S L G V	Bacillus subtilis
	317	K Y I D I G P V N K T V N M L C V W D R	Dictyostelium discoideum
	266	W G G I I P A M L N S L L A L K V L G Y	Synechocystis sp. PCC 6803
	286	W G G I Q P P A V Y S V I A L Y L L G Y	Streptomyces coelicolor A3
15		T - Q H P A F I K G L E G L E L Y G V E	Majority
		-----+-----	
		350 360	
		-----+-----	
	278	T - Q H P A F I K G W E G L E L Y G V E	A. acidocaldarius ATCC27009
20	278	T - Q H P A F I K G W E G L E L Y G V E	A. acidocaldarius JCM 5260T
	278	T - D H P A F V K G F E G L E A Y G V H	A. acidoterrestris DSM 3902
	279	S R Y S P I I R R A I T G I K S L V T K	Bacillus subtilis
	337	E G K S P A F Y K H A D R L K D Y - L W	Dictyostelium discoideum
	286	D V N D L Y V Q R G L A A I D N F A V E	Synechocystis sp. PCC 6803
25	306	D L E H P V M R A G L E S L D R F A V W	Streptomyces coelicolor A3
		L S D G G W M F Q A - S I S P V W D T G	Majority
		-----+-----	
		370 380	
		-----+-----	
30	297	L D Y G G W M F Q A - S I S P V W D T G	A. acidocaldarius ATCC27009
	297	L D Y G G W M F Q A - S I S P V W D T G	A. acidocaldarius JCM 5260T
	297	T S D G G W M F Q A - S I S P I W D T G	A. acidoterrestris DSM 3902
	299	C N G I P Y L - E N - S T S T V W D T A	Bacillus subtilis
35	356	L S F D G M K M Q G Y N G S Q L W D T A	Dictyostelium discoideum
	306	T E - D S Y A I Q A - C V S P V W D T A	Synechocystis sp. PCC 6803
	326	R E D G A R M I E A - C Q S P V W D T C	Streptomyces coelicolor A3
40		L A V L A L R A A G L P A D H P A L V K	Majority
		-----+-----	
		390 400	
		-----+-----	
	316	L A V L A L R A A G L P A D H D R L V K	A. acidocaldarius ATCC27009
	316	L A V L A L R A A G L P A D H D R L V K	A. acidocaldarius JCM 5260T
45	316	L T V L A L R S A G L P P D H P A L I K	A. acidoterrestris DSM 3902
	317	L I S Y A L Q K N G V T E T D G S V T K	Bacillus subtilis
	376	F T I Q A F M E S G I A N Q F Q D C M K	Dictyostelium discoideum
	324	W V V R A L A E A D L G K D H P A L V K	Synechocystis sp. PCC 6803
50	345	L A T I A L A D A G V P E D H P Q L V K	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		A G E W L L D R Q I T V P G D W A V K R	Majority
		-----+-----+	
5		410 420	
		-----+-----+	
	336	A G E W L L D R Q I T V P G D W A V K R	A. acidocaldarius ATCC27009
	336	A G E W L L D R Q I T V P G D W A V K R	A. acidocaldarius JCM 5260T
	336	A G E W L V S K Q I L K D G D W K V R R	A. acidoterrestris DSM 3902
10	337	A A D F L L E R Q H T K I A D W S V K N	Bacillus subtilis
	396	L A G H Y L D I S Q V P E D A R D M K H	Dictyostelium discoideum
	344	A G Q W L L D K Q I L T Y G D W Q I K N	Synechocystis sp. PCC 6803
	365	A S D W M L G E Q I V R P G D W S V K R	Streptomyces coelicolor A3
15		- - P N L K P G G W A F E F D N V N Y P	Majority
		-----+-----+	
		430 440	
		-----+-----+	
	356	- - P N L K P G G F A F Q F D N V Y Y P	A. acidocaldarius ATCC27009
20	356	- - P N L K P G G F A F Q F D N V Y Y P	A. acidocaldarius JCM 5260T
	356	- - R K A K P G G W A F E F H C E N Y P	A. acidoterrestris DSM 3902
	357	- - P N S V P G G W G F S N I N T N N P	Bacillus subtilis
	416	Y H R H Y S K G A W P F S T V D H G W P	Dictyostelium discoideum
	364	- - P H G E P G A W A F E F D N N F Y P	Synechocystis sp. PCC 6803
25	385	- - P G L P P G G W A F E F H N D N Y P	Streptomyces coelicolor A3
		D V D D T A V V V - - - L A L N G L R L	Majority
		-----+-----+	
		450 460	
		-----+-----+	
30	374	D V D D T A V V V - - - W A L N T L R L	A. acidocaldarius ATCC27009
	374	D V D D T A V V V - - - W A L N T L R L	A. acidocaldarius JCM 5260T
	374	D V D D T A M V V - - - L A L N G I Q L	A. acidoterrestris DSM 3902
	375	D C D D T T A V L - - - K A I P R N H S	Bacillus subtilis
35	436	I S D C T A E G I K S A L A L R S L P F	Dictyostelium discoideum
	382	D I D D T C V V M - - - M A L Q G I T L	Synechocystis sp. PCC 6803
	403	D I D D T A E V V - - - L A L R R V R H	Streptomyces coelicolor A3
		P D E E R R R D A I T K G F R W L L G M	Majority
		-----+-----+	
		470 480	
		-----+-----+	
40	391	P D E R R R R D A M T K G F R W I V G M	A. acidocaldarius ATCC27009
	391	P D E R R R R D A M T K G F R W I V G M	A. acidocaldarius JCM 5260T
	391	P D E G K R R D A L T R G F R W L R E M	A. acidoterrestris DSM 3902
45	392	P A A W - - - - - E R G V S W L L S M	Bacillus subtilis
	456	I E P I S L D R - I A D G I N V L L T L	Dictyostelium discoideum
	399	P D E E R K Q G A I N K A L Q W I A T M	Synechocystis sp. PCC 6803
	420	H D P E R V E K A I G R G V R W N L G M	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		Q S S N G G W G A Y D V D N T S D L P N	Majority
		-----+-----	
5		490 500	
		-----+-----	
	411	Q S S N G G W G A Y D V D N T S D L P N	A. acidocaldarius ATCC27009
	411	Q S S N G G W G A Y D V D N T S D L P N	A. acidocaldarius JCM 5260T
	411	Q S S N G G W G A Y D V D N T R Q L T K	A.acidoterrestris DSM 3902
10	406	Q N N D G G F S A F E K N V N H P L I R	Bacillus subtilis
	475	Q N G D G G W A S Y E N T R G P K W L E	Dictyostelium discoideum
	419	Q C K T G G W A A F D I D N D Q D W L N	Synechocystis sp. PCC 6803
	440	Q S K N G A W G A F D V D N T S A F P N	Streptomyces coelicolor A3
		H L P - F C D F G E V - I D P P S A D V	Majority
15		-----+-----	
		510 520	
		-----+-----	
	431	H I P - F C D F G E V - T D P P S E D V	A. acidocaldarius ATCC27009
	431	H I P - F C D F G E V - T D P P S E D V	A. acidocaldarius JCM 5260T
20	431	S D S I F A T S G E V - I D P P S E D V	A.acidoterrestris DSM 3902
	426	L L P L E S A E D A A - V D P S T A D L	Bacillus subtilis
	495	K F N P S E V F Q N I M I D Y S Y V E C	Dictyostelium discoideum
	439	Q L P - Y G D L K A M - I D P S T A D I	Synechocystis sp. PCC 6803
	460	R L P - F C D F G E V - I D P P S A D V	Streptomyces coelicolor A3
25		T A H V L E C L G S - - - F G - - - -	Majority
		-----+-----	
		530 540	
		-----+-----	
30	449	T A H V L E C F G S - - - F G - - - -	A. acidocaldarius ATCC27009
	449	T A H V L E C F G S - - - F G - - - -	A. acidocaldarius JCM 5260T
	450	T A H V L E C F G S - - - F G - - - -	A.acidoterrestris DSM 3902
	445	T G R V L H F L G E - - K V G - - - -	Bacillus subtilis
	515	S A A C I Q A M S A F R K H A P N H P R	Dictyostelium discoideum
35	457	T A R V V E M L G A - - - C G - - - -	Synechocystis sp. PCC 6803
	478	T A H V V E M L A V - - - E G - - - -	Streptomyces coelicolor A3
		Y D E A W K V I R R A V E Y L K R E Q E	Majority
		-----+-----	
40		550 560	
		-----+-----	
	461	Y D D A W K V I R R A V E Y L K R E Q K	A. acidocaldarius ATCC27009
	461	Y D D A W K V I R R A V E Y L K R E Q K	A. acidocaldarius JCM 5260T
	462	Y D E A W K V I R K A V E Y L K A Q Q R	A.acidoterrestris DSM 3902
45	458	F T E K H Q H I Q R A V K W L F E H Q E	Bacillus subtilis
	535	I K E I N R S I A R G V K F I K S I Q R	Dictyostelium discoideum
	469	L T M D S P R V E R G L T Y L L Q E Q E	Synechocystis sp. PCC 6803
	490	L A H D P R T - R R G I Q W L L D A Q E	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		Q D G S W F G R W G V N Y L Y G T G A V	Majority
		-----+-----+	
5		570 580	
		-----+-----+	
	481	P D G S W F G R W G V N Y L Y G T G A V	A. acidocaldarius ATCC27009
	481	P D G S W F G R W G V N Y L Y G T G A V	A. acidocaldarius JCM 5260T
	482	P D G S W F G R W G V N Y V Y G I G A V	A. acidoterrestris DSM 3902
10	478	Q N G S W Y G R W G V C Y I Y G T W A A	Bacillus subtilis
	555	Q D G S W L G S W G I C F T Y G T W F G	Dictyostelium discoideum
	489	Q D G S W F G R W G V N Y L Y G T S G A	Synechocystis sp. PCC 6803
	509	T D G S W F G R W G V N Y V Y G T G S V	Streptomyces coelicolor A3
15		V S A L K A V G L D T R E P Y I Q K A L	Majority
		-----+-----+	
		590 600	
		-----+-----+	
	501	V S A L K A V G I D T R E P Y I Q K A L	A. acidocaldarius ATCC27009
20	501	V S A L K A V G I D T R E P Y I Q K A L	A. acidocaldarius JCM 5260T
	502	V P G L K A V G V D M R E P W V Q K S L	A. acidoterrestris DSM 3902
	498	L T G M H A C G L T E S I P V Y K R L C	Bacillus subtilis
	575	I E G L V A S G E P L T S P S I V K A C	Dictyostelium discoideum
	509	L S A L A I Y D A Q R F A P Q I K T A I	Synechocystis sp. PCC 6803
25	529	I P A L T A A G L P T S H P A I R R A V	Streptomyces coelicolor A3
		D W L E S H Q N A D G G W G E D C R S Y	Majority
		-----+-----+	
		610 620	
		-----+-----+	
30	521	D W V E Q H Q N P D G G W G E D C R S Y	A. acidocaldarius ATCC27009
	521	D W V E Q H Q N P D G G W G E D C R S Y	A. acidocaldarius JCM 5260T
	522	D W L V E H Q N E D G G W G E D C R S Y	A. acidoterrestris DSM 3902
	518	V - - - - - - - - - - G S N P Y	Bacillus subtilis
35	595	K F L A S K Q R A D G G W G E S F K S -	Dictyostelium discoideum
	529	A W L L S C Q N A D G G W G E T C E S Y	Synechocystis sp. PCC 6803
	549	R W L E S V Q N E D G G W G E D L R S Y	Streptomyces coelicolor A3
		E - D P E Y A G Q G A S T A S Q T A W A	Majority
		-----+-----+	
40		630 640	
		-----+-----+	
	541	E - D P A Y A G K G A S T P S Q T A W A	A. acidocaldarius ATCC27009
	541	E - D P A Y A G K G A S T P S Q T A W A	A. acidocaldarius JCM 5260T
45	542	D - D P R L A G Q G V S T P S Q T A W A	A. acidoterrestris DSM 3902
	524	K M M T E - A G E N P A K A P K S K - -	Bacillus subtilis
	614	N V T K E Y V Q H E T S Q V V N T G W A	Dictyostelium discoideum
	549	K - N K Q L K G Q G N S T A S Q T A W A	Synechocystis sp. PCC 6803
	569	R Y V R E W S G R G A S T A S Q T G W A	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		L M A L I A G - - - - - G R A E - -	Majority
		-----+-----	
5		650 660	
		-----+-----	
	560	L M A L I A G - - - - - G R A E - -	A. acidocaldarius ATCC27009
	560	L M A L I A G - - - - - G R A E - -	A. acidocaldarius JCM 5260T
	561	L M A L I A G - - - - - G R V E - -	A. acidoterrestris DSM 3902
10	541	- - - - -	Bacillus subtilis
	634	L L S L M S A - K Y P D R - - - - -	Dictyostelium discoideum
	568	L I G L L D A L K Y L P S L G Q D A K L	Synechocystis sp. PCC 6803
	589	L M A L L A A - - - - - G E R D - -	Streptomyces coelicolor A3
15		S E A A E R G V A Y L V E T Q R P D G G	Majority
		-----+-----	
		670 680	
		-----+-----	
	571	S E A A R R G V Q Y L V E T Q R P D G G	A. acidocaldarius ATCC27009
20	571	S E A A R R G V Q Y L V E T Q R P D G G	A. acidocaldarius JCM 5260T
	572	S D A V L R G V T Y L H D T Q R A D G G	A. acidoterrestris DSM 3902
	541	- - - - -	Bacillus subtilis
	646	- E C I E R G I K F L I Q R Q Y P N G D	Dictyostelium discoideum
	588	T T A I E G G V A F L V Q G Q T P K G T	Synechocystis sp. PCC 6803
25	600	S K A V E R G V A W L A A T Q R E D G S	Streptomyces coelicolor A3
		W D E P Y Y T G T G F P G D F Y L G Y T	Majority
		-----+-----	
		690 700	
		-----+-----	
30	591	W D E P Y Y T G T A S P G D F Y L G Y T	A. acidocaldarius ATCC27009
	591	W D E P Y Y T G T G F P G D F Y L G Y T	A. acidocaldarius JCM 5260T
	592	W D E E V Y T G T G F P G D F Y L A Y T	A. acidoterrestris DSM 3902
	541	- - - - -	Bacillus subtilis
35	665	F P Q E S I I G V - F N F N C M I S Y S	Dictyostelium discoideum
	608	W E E A E Y T G T G F P C H F Y I R Y H	Synechocystis sp. PCC 6803
	620	W D E P Y F T G T G F P W D F S I N Y N	Streptomyces coelicolor A3
40		M Y R Q V F P L L A L G R Y K Q A - - -	Majority
		-----+-----	
		710 720	
		-----+-----	
	611	M Y R H V F P T L A L G R Y K Q A - - -	A. acidocaldarius ATCC27009
	611	M Y R H V F P T L A L G R Y K Q A - - -	A. acidocaldarius JCM 5260T
45	612	M Y R D I L P V W A L G R Y Q E A - - -	A. acidoterrestris DSM 3902
	542	M Y R F I - - - - - E E P L	Bacillus subtilis
	684	N Y K N I F P L W A L S R Y N Q - - - L	Dictyostelium discoideum
	628	Y Y R Q Y F P L I A L A R Y S H L Q A -	Synechocystis sp. PCC 6803
	640	L Y R Q V F P L T A L G R Y V H G E P F	Streptomyces coelicolor A3

Figure 6: Shc amino acid sequence alignments (continued)

		- - - - - E R - G Majority	
		+-----+	
5		730 740	
		+-----+	
	628	- - - - - I E R R	A. acidocaldarius ATCC27009
	628	- - - - - I E R R	A. acidocaldarius JCM 5260T
	629	- - - - - M Q R I R	A. acidoterrestris DSM 3902
10	551	Y K R P - - - - - G	Bacillus subtilis
	701	Y L K S K - - - - -	Dictyostelium discoideum
	647	- - - - -	Synechocystis sp. PCC 6803
	660	A K K P R A A D A P A E A A P A E V K G	Streptomyces coelicolor A3
15		S Majority	
		--	
		--	
	631		A. acidocaldarius ATCC27009
20	631		A. acidocaldarius JCM 5260T
	634	G	A. acidoterrestris DSM 3902
	556	L	Bacillus subtilis
	706	I	Dictyostelium discoideum
	647	S	Synechocystis sp. PCC 6803
25	680	S	Streptomyces coelicolor A3

Figure 7

1 50
Z.bali sequencing (1) -----TGCATGGCCGTTCTTAGTTGGT
sacc. humal (1) --CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
cand. coll (1) --CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
grape (1) --CTCTTTCTTGATTTCTATGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
zygo. ruxil (1) --CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
PD sequencing (1) ----GTGCTGGAA--TTCGGCT---TTGCATGGCCGTTCTTAGTTGGT
BF sequencing (1) ----TGCCTGGAA--TTCGGCT---TTGCATGGCCGTTCTTAGTTGGT
pen. cry (1) ---TCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
a. nidu (1) AGCTCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
euro. amst (1) ----TTCCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
asp. cand (1) --CTCTTTCTTGATCTTTTGGATGGTGGTGCATGGCCGTTCTTAGTTGGT
chicken (1) --CTCTTTCTCGATTCCGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
wheat (1) --CTCTTTCTTGATCTTATGGGTGGTGGTGCATGGCCGTTCTTAGTTGGT
Consensus (1) CTCTTTCTTGAT TT TGG TGGTGGTGCATGGCCGTTCTTAGTTGGT
51 100
Z.bali sequencing (23) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTTAACCTACT
sacc. humal (49) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTTAACCTACT
cand. coll (49) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTTAACCTACT
grape (49) GGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTCAGCCTGCT
zygo. ruxil (49) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTTAACCTACT
PD sequencing (40) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTCGGCCCT-T
BF sequencing (39) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTCGGCCCT-T
pen. cry (48) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTCGGCCCT-T
a. nidu (51) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTCGGCCCT-T
euro. amst (46) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTCGGCCCT-T
asp. cand (49) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTCGGCCCT-T
chicken (49) GGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACTCTGGCATGCT
wheat (49) GGAGCGATTTGTCTGGTTAATTCGGTTAACGAACGAGACCTCAGCCTGCT
Consensus (51) GGAGTGATTTGTCTGCTTAATTGCCGATAACGAACGAGACCTCGGCCCT CT
101 150
Z.bali sequencing (73) AAATAGT--GGTGCTA-GCATTGCTGGTTTTTCCACTTCTTAGAGGGAC
sacc. humal (99) AAATAGT--GGTGCTA-GCATTGCTGGTTAT-CCACTTCTTAGAGGGAC
cand. coll (99) AAATAGT--GGTGCTA-GCATTGCTGGTTAT-CCACTTCTTAGAGGGAC
grape (99) AACTAGCTATGTGAAG-GTGAGCCTCCGCAGC-CAGCTTCTTAGAGGGAC
zygo. ruxil (99) AAATAGT--GGTGCTA-GCATTGCTGGTTTTTCCACTTCTTAGAGGGAC
PD sequencing (89) AAATAGCCCCGGTCC--GCATTGCGGGGCGC-TGGCTTCTTAGGGGGAC
BF sequencing (88) AAATAGCCCCGGTCC--GCGTTTGGGGGCGC-TGGCTTCTTAGGGGGAC
pen. cry (97) AAATAGCCCCGGTCC--GCATTGCGGGGCGC-TGGCTTCTTAGGGGGAC
a. nidu (100) AAATAGCCCCGGTCC--GCGTCCGGGGGCGC-TGGCTTCTTAGGGGGAC
euro. amst (95) AAATAGCCCCGGTCC--GCATTGCGGGGCGC-TGGCTTCTTAGGGGGAC
asp. cand (98) AAATAGCCCCGGTCC--GCATTGCGGGGCGC-TGGCTTCTTAGGGGGAC
chicken (99) AACTAGTTACGCGACCCCGAGCGGTCCGGCTCCAACCTCTTAGAGGGAC
wheat (99) AACTAGCTATGCGGAG-CCATCCCTCCGCAGC-TAGCTTCTTAGAGGGAC
Consensus (101) AAATAGC GGTGC GCATTGCG GCGCGC T GCTTCTTAGAGGGAC

GTGGTGCTAGCATTTGCTG Yeast prime up

CCGCTGGCTTCTTAGGG

Mold prime up

Figure 7 (continued)

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151                                200
Z.bali sequencing (121) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
sacc. humal (145) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
cand. coll (145) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
grape (147) TATGGCCGCTTAGGCCAAGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
zygo. ruxil (146) TATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
PD sequencing (135) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
BF sequencing (134) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTAATGC
pen. cry (143) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
a. nidu (146) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
euro. amst (141) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
asp. cand (144) TATCGGCT-CAAGCCGATGGAAGTGCGCGGCAATAACAGGTCTGTGATGC
chicken (149) AAGTGGCGTTTCAGCC-ACCCGAGATTGAG-CAATAACAGGTCTGTGATGC
wheat (147) TATCGCGGTTTAGGCGACGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
Consensus (151) TATCGGCT CAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC
201                                250
Z.bali sequencing (171) CCTTAGACGTTCTGGGCCGACGCGCGCTACACTGACGGAGCCAGCGAGT
sacc. humal (195) CCTTAGACGTTCTGGGCCGACGCGCGCTACACTGACGGAGCCAGCGAGT
cand. coll (195) CCTTAGACGTTCTGGGCCGACGCGCGCTACACTGACGGAGCCAGCGAGT
grape (197) CCTTAGATGTTCTGGGCCGACGCGCGCTACACTGATGTATTCAACGAGT
zygo. ruxil (196) CCTTAGACGTTCTGGGCCGACGCGCGCTACACTGACGGAGCCAGCGAGT
PD sequencing (184) CCTTAGATGTTCTGGGCCGACGCGCGCTACACTGACAGGGCCAGCGAGT
BF sequencing (183) CCTTAGATGTTCTGGGCCGACGCGCGCTACACTGACAGGGCCAGCGGGT
pen. cry (192) CCTTAGATGTTCTGGGCCGACGCGCGCTACACTGACAGGGCCAGCGAGT
a. nidu (195) CCTTAGATGTTCTGGGCCGACGCGCGCTACACTGACAGGGCCAGCGAGT
euro. amst (190) CCTTAGATGTTCTGGGCCGACGCGCGCTACACTGACAGGGCCAGCGAGT
asp. cand (193) CCTTAGATGTTCTGGGCCGACGCGCGCTACACTGACAGGGCCAGCGAGT
chicken (197) CCTTAGATGTTCTGGGCCGACGCGCGCTACACTGACTGGCTCAGCTTGT
wheat (197) CCTTAGATGTTCTGGGCCGACGCGCGCTACACTGATGTATTCAACGAGT
Consensus (201) CCTTAGATGTTCTGGGCCGACGCGCGCTACACTGAC GGGCCAGCGAGT
251                                300
Z.bali sequencing (221) CTA-ACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCTGTGC
sacc. humal (245) CTA-ACCTTGGCCGAGAGGTCTTGGTAATCTTGTGAAACTCCGTCTGTGC
cand. coll (245) CTA-ACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCTGTGC
grape (247) CTATAGCCTTGGCCGACAGGCCCGGGTAATCTTGTGAAACTCCGTCTGTGC
zygo. ruxil (246) CTA-ACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCTGTGC
PD sequencing (234) ACATCACCTTAACCGAGAGGTCTGGGTAATCTTGTAAACCCGTCTGTGC
BF sequencing (233) ACATCACCTTGGCCGAGAGGTCTGGGTAATCTTGTAAACCCGTCTGTGC
pen. cry (242) ACATCACCTTAACCGAGAGGTCTGGGTAATCTTGTAAACCCGTCTGTGC
a. nidu (245) ACATCACCTTGGCCGAGAGGCCCGGGTAATCTTGTAAACCCGTCTGTGC
euro. amst (240) ACATCACCTTAACCGAGAGGTCTGGGTAATCTTGTAAACCCGTCTGTGC
asp. cand (243) ACATCACCTTGGCCGAGAGGTCTGGGTAATCTTGTAAACCCGTCTGTGC
chicken (247) GTCTACCCCTACGCCGGCAGGCGCGGGTAACCCGTGAAACCCATTCTGTGA
wheat (247) ATATAGCCCTGGCCGACAGGCCCGGGTAATCTTGGGAAATTTTCATCGTGA
Consensus (251) ATAT ACCTTGGCCGAGAGGTCTGGGTAATCTTGT AAACCC GTCGTGC

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GGAGCCAGCGAGTCTAAC Yeast primer low
AGGGCCAGCGAGTACATCA Mold primer low
CGGTTTCAAGCCGATGGAAGT Yeast probe
CTCAAGCCGATGGAAGTGCG Mold probe

Figure 7 (continued)

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301                               350
Z.bali sequencing (269) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
sacc. humal (293) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
cand. coll (293) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
grape (296) TGGGGATA-----
zygo. ruxil (294) TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAA
PD sequencing (284) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
BF sequencing (283) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
pen. cry (292) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
a. nidu (295) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
euro. amst (290) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
asp. cand (293) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTAG
chicken (297) TGGGGATCGGGGATTGCAATTATCCCATGAACGAGGAATCCCAGTAA
wheat (297) TGGGGATAGATCATGCAATTGTTGGTCTTCAACGAGGAATGCCTAGTAA
Consensus (301) TGGGGATAGAGCATTGCAATTATTGCTCTTCAACGAGGAATGCCTAGTA
351                               400
Z.bali sequencing (319) GCGCAAGTCATCAACTTGCCTTGATTACGTCCCTGCCCTTTGTACACACA
sacc. humal (343) GCGCAAGTCATCAGCTTGCCTTGATTACGTCCCTGCCCTTTGTACACACC
cand. coll (343) GCGCAAGTCATCAGCTTGCCTTGATTACGTCCCTGCCCTTTGTACACACC
grape (304) -----
zygo. ruxil (344) GCGCAAGTCATCAGCTTGCCTTGATTACGTCCCTGCCCTTTGTACACACC
PD sequencing (334) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACA
BF sequencing (333) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACA
pen. cry (342) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
a. nidu (345) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
euro. amst (340) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
asp. cand (343) GCACGAGTCATCAGCTCGTGCCGATTACGTCCCTGCCCTTTGTACACACC
chicken (347) GTGCGGGTCATAAGCTCGCGTTGATTAAAGTCCCTGCCCTTTGTACACACC
wheat (347) GCGCGAGTCATCAGCTCGCGTTGACTACGTCCCTGCCCTTTGTACACACC
Consensus (351) GC CGAGTCATCAGCTCG G GATTACGTCCCTGCCCTTTGTACACACC
401                               450
Z.bali sequencing (369) AGCCGAAT-----
sacc. humal (393) GCGCGTCGCTAG-----
cand. coll (393) GCGCGTCGCTAGTACC-----
grape (304) -----
zygo. ruxil (394) GCGCGTCGCTAGTA-----
PD sequencing (384) AGCCGA--ATT-----
BF sequencing (383) AGCCGA--ATTCTGCAGATA-----
pen. cry (392) GCGCGTCGCTACTACCGATTGAATG-----
a. nidu (395) GCGCGTCGCTAC-----
euro. amst (390) GCGCGTCGCTACTACCGATTGAATGGCTCGGTGAGGCC-----
asp. cand (393) GCGCGTCGCTACTACCGATTGAATGGCTCGGTGAGGCCTCCGGACTGGCT
chicken (397) GCGCGTCGCTA-----
wheat (397) GCGCGTCGCTC-----
Consensus (401) GCGCGTCGCTA

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Alignment 2

-	A	G	A	G	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	A	C	G	C	Consensus #1
.	Consensus #1
-	A	G	A	G	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	A	C	G	C	Majority

10 20 30

1	-	A	G	A	G	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C
1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	G	A	C	G	C	
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C
1	G	A	G	-	-	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C
1	-	A	G	A	G	T	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C
1	G	A	G	A	G	C	T	T	G	A	T	C	C	T	G	G	C	T	C	A	G	G	A	C	G	C

T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	G	A	G	Consensus #1
T	G	G	C	G	G	C	G	T	G	C	C	T	A	A	.	A	C	A	T	G	C	A	A	G	T	C	G	.	.	Consensus #1
T	C	G	C	G	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	G	T	C	G	A	G	Majority

40 50 60

30	T	G	G	C	G	G	T	G	C	C	T	A	A	T	A	C	A	T	G	G	A	A	T	C	G	A	G	
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	T	C	G	A	G
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	T	C	G	A	G
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	T	C	G	A	G
10	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	T	C	G	A	G
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	T	C	G	A	G
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	T	C	G	A	G
29	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	T	C	G	A	G
30	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	T	C	G	A	G
31	T	G	G	C	G	C	G	T	G	C	C	T	A	A	T	A	C	A	T	G	C	A	A	T	C	G	-	-

Day, September 1954	Consensus #1	Consensus #1	Majority
C G G A C - - C . C T T C G G . G - - - - -	Consensus #1	Consensus #1	Majority
.	Consensus #1	Consensus #1	Majority
C G G A C - - C - C T T C G G A G - - - - -	Consensus #1	Consensus #1	Majority

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	
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	100	110	120	
75	- - - - -	A G C C G G C G G A C C G G G T G	43030 16S	
75	- - - - -	A G C C G G C G G A C C G G G T G	genbank 16S 43030 AB059664	
73	- - - - -	A G C C G G C G G A C C G G G T G	49029 16S	
73	- - - - -	A G C C G G C G G A C C G G G T G	genbank 16S 49029 AB042059	
53	- - - - -	A G C C G G C G G A C C G G G T G	cc-4902516SRDNA-t7p_C02_006-1-ed	
73	- - - - -	A G C C G G C G G A C C G G G T G	genbank 16S 49025 AB042058	
90	A A G A G A G G T T A C T T	A G C C G G C G G A C C G G G T G	Clostridium elmenteitii	
85	- - - - -	A G C C G G C G G A C C G G G T G	Geobacillus subterraneus 16S AF276307	
75	- - - - -	A G C C G G C G G A C C G G G T G	Sulfobacillus disulfidooxidans 16S U349	
83	- - - - -	A G C C G G C G G A C C G G G T G	Bacillus thermoleovorans ribosomal RNA	

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	.	.	C	A	G	A	C	Consensus #1	
93	A	G	.	A	A	C	.	C	G	T	G	G	G	.	A	A	.	C	.	C	C	Consensus #1	
93	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	Majority
91	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	
91	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	
71	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	
91	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	
71	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	
91	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	
120	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	
106	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	
93	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	
104	A	G	T	A	A	C	A	C	G	T	G	G	G	C	A	A	T	C	T	G	C	C	T	T	T	C	A	G	A	C	

43030 16s

genbank 16s 43030 AB059664

49029 16s

genbank 16s 49029 AB042059

cc-4902516SRDNA-t7p_C02_006-1-ed

genbank 16s 49025 AB042058

Clostridium elmenteitii

Geobacillus subterraneus 16S AF276307

Sulfobacillus disulfidooxidans 16S U349

Bacillus thermoleovorans ribosomal RNA

43030 16S
 genbank 16s 43030 AB059664
 49029 16S
 genbank 16s 49029 AB042059
 cc-4902516SRDNA-t7p_C02_006-1-ed
 genbank 16s 49025 AB042058
 Clostridium elmenteitii
 Geobacillus subterraneus 16S AF276307
 Sulfolobacillus disulfidooxidans 16S U349
 Bacillus thermoleovorans ribosomal RNA

123	C	G	G	A	A	T	A	A	C	C	C	C	G	A	A	C	G	G	G	C	G	C	T	A	A	T	G	43030 16S	
123	C	G	G	A	A	T	A	A	C	C	C	C	G	G	A	A	C	G	G	C	G	C	T	A	A	T	G	genbank 16S 43030 AB059664	
121	C	G	G	A	A	T	A	A	C	C	C	C	T	G	A	A	C	G	G	T	G	C	T	A	A	T	G	49029 16S	
121	C	G	G	A	A	T	A	A	C	C	C	T	G	G	A	A	C	G	G	T	G	C	T	A	A	T	G	genbank 16S 49029 AB042059	
101	T	G	G	A	A	T	A	A	C	C	T	C	C	G	A	A	C	G	G	T	G	C	T	A	A	T	G	cc-4902516SRDNA-t7p_C02_006-1-ed	
121	T	G	G	A	A	T	A	A	C	C	T	C	C	G	A	A	C	G	G	T	G	C	T	A	A	T	G	genbank 16S 49025 AB042058	
150	G	G	G	A	A	T	A	A	C	A	T	T	G	G	A	A	C	C	A	G	T	G	C	T	A	A	T	A	Clostridium elmenteitii
136	C	G	G	A	A	T	A	A	C	T	C	C	G	G	A	A	C	C	G	G	A	G	C	T	A	A	T	A	Geobacillus subterraneus 16S AF276307
123	T	G	G	A	A	T	A	A	C	G	C	C	T	G	A	A	C	G	G	T	G	C	T	A	A	T	G	G	Sulfobacillus disulfidooxidans 16S U34
134	C	G	G	A	A	T	A	A	C	T	C	C	G	G	A	A	C	C	G	G	A	G	C	T	A	A	T	A	Bacillus thermoleovorans ribosomal RNA

43030 16S
 genbank 16s 43030 AB059664
 49029 16S
 genbank 16s 49029 AB042059
 cc-4902516SRDNA-t7p_C02_006-1-ed
 genbank 16s 49025 AB042058
 Clostridium elmenteitii
 Geobacillus subterraneus 16S AF276307
 Sulfolobacillus disulfidooxidans 16S U349
 Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

C	C	G	G	A	T	A	-	.	.	.	C	.	C	G	A	G	.	A	G	G	C	A	T	C	T	.	C	T	T		Consensus #1	
C	C	.	.	A	T	A	G	C	.	T	Consensus #1
C	C	G	G	A	T	A	-	A	C	C	C	G	C	G	A	G	A	G	G	C	A	T	C	T	T	C	T	T		Majority		

G	.	G	G	.	G	A	A	G	G	T	G	-	C	A	A	.	T	G	-	.	A	T	C	G	C	T	G		Consensus #1	
.	G	.	A	A	G	G		Consensus #1
G	C	G	G	G	G	A	A	G	G	T	G	-	C	A	A	T	T	G	-	.	C	A	T	C	G	C	T	G		Majority

183	G	C	G	G	G	G	G	G	G	A	A	G	G	C	C	-	C	A	A	T	T	G	-	G	G	T	G	G	C	T	G	43030 16s	
183	G	C	G	G	G	G	G	G	G	A	A	G	G	C	C	-	C	A	A	T	T	G	-	G	G	C	T	G	G	C	T	G	genbank 16s 43030 AB059664
180	G	C	T	G	G	G	G	G	G	A	A	G	G	T	G	-	C	A	A	G	T	G	-	C	A	C	G	C	A	G	G	49029 16s	
180	G	C	T	G	G	G	G	G	G	A	A	G	G	T	G	-	C	A	A	G	T	G	-	C	A	C	G	C	A	G	G	genbank 16s 49029 AB042059	
160	G	T	G	T	T	G	G	G	G	A	A	G	G	A	T	G	-	C	A	A	C	T	G	-	C	A	T	G	G	C	T	G	cc-4902516SRDNA-t7p_C02_006-1-ed
180	G	T	G	T	T	G	G	G	G	A	A	G	G	A	T	G	-	C	A	A	C	T	G	-	C	A	T	G	G	C	T	G	genbank 16s 49025 AB042058
210	A	T	A	G	A	G	A	G	A	G	A	G	A	T	-	T	T	A	T	C	G	-	G	-	A	T	C	A	-	-	-	-	Clostridium elmenteitii
195	C	G	G	T	T	G	A	G	G	C	G	G	C	C	T	T	T	T	T	G	G	C	T	G	T	C	A	C	T	T	Geobacillus subterraneus 16S AF276307		
182	T	G	T	G	G	G	A	A	G	A	T	G	-	C	T	A	C	G	G	-	-	C	A	T	C	G	C	C	A	Sulfobacillus disulfidooxidans 16S U34			
193	T	G	T	T	G	A	A	G	G	C	G	G	C	-	T	T	T	G	G	-	G	C	T	G	T	A	C	T	T	Bacillus thermoleovorans ribosomal RNA			

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

	Consensus #1																											
	Consensus #1																											
	Majority																											
	A	.	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T	
	.	.	G	A	.	G	.	G	C	C	C	G	C	G	.	C	.	A	T	T	A	G	C	T	.	G	T	T
	A	G	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T	
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	N	G	T	T
	A	T	G	A	G	A	G	A	G	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	G	G	T	T
	A	T	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A	G	C	C	C	G	C	G	C	G	C	A	T	T	A	G	C	T	A	G	T	T
	A	G	A	G	A	G	A</																					

G	G	T	G	.	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	Consensus #1
G	G	.	.	.	G	G	T	A	A	C	G	G	.	.	.	A	C	C	A	A	G	G	C	.	.	.	G	A	T	Consensus #1
G	G	T	G	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	Majority	

G	G	C	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	43030 16s
G	G	C	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	genbank 16s 43030 AB059664
G	G	T	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	49029 16s
G	G	T	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	G	A	T	genbank 16s 49029 AB042059
G	G	T	G	A	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	T	cc-4902516SRDNA-t7p_C02_006-1-ed
G	G	T	G	A	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	T	genbank 16s 49025 AB042058
G	G	T	A	A	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	C	T	T	T	Clostridium elmenteitii
G	G	T	G	A	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	T	Geobacillus subterraneus 16S AF276307
G	G	T	G	A	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	T	Sulfobacillus disulfidooxidans 16S U349
G	G	T	G	A	G	G	T	A	A	C	G	G	C	T	C	A	C	C	A	A	G	G	C	G	A	C	T	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

G C G T A G C C G A C C T G A G A G G T G A C C G G C C A Consensus #1
. . G T A G C C G . C C T G A G A G G T G . . C G G C C A Consensus #1
G C G T A G C C G A C C T G A G A G G T G A C C G G C C A Majority

270 G C G T A G C C G A C C T G A G A G G T G A C C G G C C A 330 43030 16s
270 G C G T A G C C G A C C T G A G A G G T G A C C G G C C A genbank 16s 43030 AB059664
267 G C G T A G C C G A C C T G A G A G G T G A C C G G C C A 49029 16s
267 G C G T A G C C G A C C T G A G A G G T G A C C G G C C A genbank 16s 49029 AB042059
247 G C G T A G C C G A C C T G A G A G G T G A C C G G C C A cc-4902516SRDNA-t7p_C02_006-1-ed
267 G C G T A G C C G A C C T G A G A G G T G A C C G G C C A genbank 16s 49025 AB042058
291 C A G T A G C C G A C C T G A G A G G T G A C C G G C C A Clostridium elmenteitii
285 G C G T A G C C G A C C T G A G A G G T G A C C G G C C A Geobacillus subterraneus 16S AF276307
269 G C G T A G C C G A C C T G A G A G G T G A C C G G C C A Sulfolobacillus disulfidooxidans 16S U349
282 G C G T A G C C G A C C T G A G A G G T G A C C G G C C A Bacillus thermoleovorans ribosomal RNA

C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T Consensus #1
C A C T G G . A C T G A G A C A C G G . C C A G A C T C C T Consensus #1
C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T Majority

300 C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T 360 43030 16s
300 C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T genbank 16s 43030 AB059664
297 C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T 49029 16s
297 C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T genbank 16s 49029 AB042059
277 C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T cc-4902516SRDNA-t7p_C02_006-1-ed
297 C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T genbank 16s 49025 AB042058
321 C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T Clostridium elmenteitii
315 C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T Geobacillus subterraneus 16S AF276307
299 C A C T G G G A C T G A G A C A C G G C C C A G A C T C C T Sulfolobacillus disulfidooxidans 16S U349
312 G A C T G G G A C T G A G A C A C G G C C C A G A C T C C T Bacillus thermoleovorans ribosomal RNA

Alignment Report of Ali 16S alignment.meq ClustalV (Weighted)

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	Consensus #1	Consensus #1
A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A	Consensus #1	Consensus #1
A C G G G A G G C A G C A G T . G G G A A T . T T . C . C A	Consensus #1	Consensus #1
A C G G G A G G C A G C A G T A G G G A A T C T T C C G C A	Consensus #1	Consensus #1

330	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	G	C	A	43030 16s	
330	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	G	C	A	genbank 16s 43030 AB059664	
327	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	G	C	A	49029 16s	
327	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	G	C	A	genbank 16s 49029 AB042059	
307	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	G	C	A	cc-4902516SRDNA-t7p_C02_006-1-ed	
327	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	G	C	A	genbank 16s 49025 AB042058	
351	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	G	G	G	G	A	A	T	A	T	T	G	C	C	A	Clostridium elmenteitii	
345	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	C	G	C	A	Geobacillus subterraneus 16S AF276307
329	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	C	G	C	A	Sulfobacillus disulfidooxidans 16S U349
342	A	C	G	G	G	A	G	G	C	A	G	C	A	G	T	A	G	G	G	A	A	T	C	T	T	C	C	G	C	A	Bacillus thermoleovorans ribosomal RNA

A T G G G C G C A A G C C T G A C G G A G C A A C G C C G C Consensus #1
A T G G . . G . A A . . C T G A . G . A G C . A C G C C G C Consensus #1
A T G G G C G C A A G C C T G A C G G A G C A A C G C C G C Majority

360 43030 16s
360 genbank 16s 43030 AB059664
357 49029 16s
357 genbank 16s 49029 AB042059
337 cc-4902516SRDNA-t7p_C02_006-1-ed
357 genbank 16s 49025 AB042058
381 Clostridium elmenteitii
375 Geobacillus subterraneus 16S AF276307
359 Sulfolobacillus disulfidooxidans 16S U349
372 Bacillus thermoleovorans ribosomal RNA

Alignment 2

	Consensus #1	Consensus #1	Consensus #1	Majority
G T G A G C G A G A A G G C C T T C G G G T T G T A A A G				
G T . A G C G A G A A G G C C T T C G G G T . G T A A A G				
G T G A G C G A G A A G G C C T T C G G G T T G T A A A G				

390	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
390	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
387	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
387	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
367	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
387	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
411	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	C	G	T	A	A	A	G	430	440	450
405	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	C	G	T	A	A	A	G	430	440	450
389	G	T	A	A	C	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	T	G	T	A	A	A	G	430	440	450
402	G	T	G	A	G	C	G	A	A	G	A	G	G	C	C	T	T	C	G	G	G	T	C	G	T	A	A	A	G	430	440	450

C	T	C	T	G	T	T	G	C	T	C	G	G	A	-	A	G	A	G	C	G	G	C	A	.	G	G	.	G		Consensus #1
C	T	.	.	G	T	G	G	A	G	Consensus #1
C	T	C	T	G	T	T	G	C	T	C	G	G	A	-	A	G	A	G	C	G	G	C	A	A	G	G	G	G		Majority

[illegible]

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

479	G T G A G G	A G A G C C C C C C C C	T A A C	C T A C G T G C C C A G	43030 16S
479	G T G A G G	A A G C C C C C C C C C	T A A C	T A C G T G C C C A G	genbank 16S 43030 AB059664
476	G A G A G G	A A G C C C C C C C C C	T A A C	T A C G T G C C C A G	49029 16S
476	G A G A G G	A A G C C C C C C C C C	T A A C	T A C G T G C C C A G	genbank 16S 49029 AB042059
456	G T G A G G	A A G C C C C C C C C C	T A A C	T A C G T G C C C A G	cc-4902516SRDNA-t7p_C02_006-1-ed
476	G T G A G G	A A G C C C C C C C C C	T A A C	T A C G T G C C C A G	genbank 16S 49025 AB042058
476	A G A G A G	A A G C C C C C C C C C	T A A C	T A C G T G C C C A G	Clostridium elmenteitii
494	A C G A G A	A A G C C C C C C C C C	T A A C	T A C G T G C C C A G	Geobacillus subterraneus 16S AF276307
477	G A G A G G	A A G C C C C C C C C C	A A C	T A C G T G C C C A G	Sulfobacillus disulfidooxidans 16S U349
491	A C G A G G	A A G C C C C C C C C C	T A A C	T A C G T G C C C A G	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

C A G C C G C G G T A A T A C G T A G G G G G C A A G C G T Consensus #1																									43030 16s																								
C A G C C G C G G T A A . A C G T A G G G G G C . A G C G T Consensus #1																									genbank 16s 43030 AB059664																								
C A G C C G C G G T A A T A C G T A G G G G G C A A G C G T Majority																									49029 16s																								
509	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	C	G	T	A	G	C	C	G	T	43030 16s																				
509	C	A	G	C	C	G	C	G	G	T	A	A	A	A	C	G	T	A	G	C	G	T	A	G	C	C	G	T	genbank 16s 43030 AB059664																				
506	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	C	G	T	A	G	C	C	G	T	49029 16s																				
506	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	C	G	T	A	G	C	C	G	T	genbank 16s 49029 AB042059																				
486	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	C	G	T	A	G	C	C	G	T	cc-4902516SRDNA-t7p_C02_006-1-ed																				
506	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	C	G	T	A	G	C	C	G	T	genbank 16s 49025 AB042058																				
506	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	C	G	T	A	G	C	C	G	T	Clostridium elmenteitii																				
524	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	C	G	T	A	G	C	C	G	T	Geobacillus subterraneus 16S AF276307																				
507	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	C	G	T	A	G	C	C	G	T	Sulfobacillus disulfidooxidans 16S U349																				
521	C	A	G	C	C	G	C	G	G	T	A	A	T	A	C	G	T	A	G	C	G	T	A	G	C	C	G	T	Bacillus thermoleovorans ribosomal RNA																				

T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Consensus #1
T	.	T	C	C	G	G	A	A	T	.	A	.	T	G	G	G	.	C	G	T	A	A	A	G	.	G	.	G	C	Consensus #1
T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Majority

539	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	43030 16S
539	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	genbank 16s 43030 AB059664
536	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	49029 16S
536	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	genbank 16s 49029 AB042059
516	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	G	G	C	G	T	A	A	A	G	C	G	T	G	cc-4902516SRDNA-t7p_C02_006-1-ed
536	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	genbank 16s 49025 AB042058
536	T	A	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Clostridium elmenteitii
554	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Geobacillus subterraneus 16S AF276307
537	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Sulfobacillus disulfidooxidans 16S U349
551	T	G	T	C	C	G	G	A	A	T	C	A	C	T	G	G	G	-	C	G	T	A	A	A	G	C	G	T	G	C	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

G T A G G C G G T T G . G T A A G T C T G . . G T G A A A G Consensus #1
G . A . G C G G G T C . G . . . T G A A A G Consensus #1
G T A G G C G G T T G C G T A A G T C T G G G G T G A A A G Majority

568	G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	43030 16s
568	G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	genbank 16s 43030 AB059664
565	G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	49029 16s
565	G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	genbank 16s 49029 AB042059
546	G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	cc-4902516SRDNA-t7p_C02_006-1-ed
565	G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	genbank 16s 49025 AB042058
565	G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	Clostridium elmenteitii
583	G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	Geobacillus subterraneus 16S AF276307
566	G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	Sulfobacillus disulfidooxidans 16S U349
580	G	T	A	G	G	C	G	G	T	T	G	.	G	T	A	A	G	T	C	T	G	.	.	G	T	G	A	A	A	G	Bacillus thermoleovorans ribosomal RNA

T C C A . G G C T C A A C C . T G G G A . . G C . T T G G A Consensus #1
. . . . G G C T C . A C C . T C . T T . G A Consensus #1
T C C A G G G C T C A A C C G T G G G A A T G C T T T G G A Majority

598	T	C	C	A	T	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	43030 16s
598	T	C	C	A	T	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	genbank 16s 43030 AB059664
595	T	C	C	A	T	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	49029 16s
595	T	C	C	A	T	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	genbank 16s 49029 AB042059
576	T	C	C	A	T	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	cc-4902516SRDNA-t7p_C02_006-1-ed
595	T	C	C	A	T	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	genbank 16s 49025 AB042058
595	G	C	T	A	C	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	Clostridium elmenteitii
595	G	C	T	A	C	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	Geobacillus subterraneus 16S AF276307
613	G	C	T	A	C	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	Sulfobacillus disulfidooxidans 16S U349
596	G	T	C	G	G	C	T	C	A	A	C	C	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	Bacillus thermoleovorans ribosomal RNA
610	C	C	C	A	C	G	G	C	T	C	A	A	C	C	.	T	G	G	G	A	.	.	G	C	.	T	T	G	G	A	

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

A A C T G C . T G - A C T T G A G T G C T G G A G A G G C A Consensus #1
 A A C T G C T T G A G T G C . G G A G A G G . . Consensus #1
 A A C T G C G T G - A C T T G A G T G C T G G A G A G G C A Majority

628	A	A	C	T	G	C	.	T	G	-	A	C	T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	C	A	43030 16s
628	A	A	C	T	G	C	.	T	G	-	A	C	T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	C	A	genbank 16s 43030 AB059664
625	A	A	C	T	G	C	.	T	G	-	A	C	T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	C	A	49029 16s
625	A	A	C	T	G	C	.	T	G	-	A	C	T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	C	A	genbank 16s 49029 AB042059
606	A	A	C	T	G	C	.	T	G	-	A	C	T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	C	N	cc-4902516SRDNA-t7p_C02_006-1-ed
625	A	A	C	T	G	C	.	T	G	-	A	C	T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	C	A	genbank 16s 49025 AB042058
624	A	A	C	T	G	C	.	T	G	-	A	C	T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	T	A	Clostridium elmenteitii
643	A	A	C	T	G	C	.	T	G	-	A	C	T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	A	G	Geobacillus subterraneus 16S AF276307
626	A	A	C	T	G	C	.	T	G	-	A	C	T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	C	A	Sulfobacillus disulfidooxidans 16S U349
640	A	A	C	T	G	C	.	T	G	-	A	C	T	T	G	A	G	T	G	C	T	G	G	A	G	A	G	G	A	G	Bacillus thermoleovorans ribosomal RNA

A G G G G A A T T C C A C G T G T - A G C G G T G . A A - T Consensus #1
 A G . . . A A T T C C . . G T G T . A . C G G T G . A A . T Consensus #1
 A G G G G A A T T C C A C G T G T - A G C G G T G A A A - T Majority

657	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G	G	T	G	.	A	A	-	T	43030 16s
657	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G	G	T	G	.	A	A	-	T	genbank 16s 43030 AB059664
654	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G	G	T	G	.	A	A	-	T	49029 16s
654	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G	G	T	G	.	A	A	-	T	genbank 16s 49029 AB042059
636	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G	G	T	G	.	A	A	-	T	cc-4902516SRDNA-t7p_C02_006-1-ed
654	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G	G	T	G	.	A	A	-	T	genbank 16s 49025 AB042058
653	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G	G	T	G	.	A	A	-	T	Clostridium elmenteitii
672	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G	G	T	G	.	A	A	-	T	Geobacillus subterraneus 16S AF276307
655	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G	G	T	G	.	A	A	-	T	Sulfobacillus disulfidooxidans 16S U349
669	A	G	G	G	G	A	A	T	T	C	C	A	C	G	T	G	T	-	A	G	C	G	G	T	G	.	A	A	-	T	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	Consensus #1
G C G . . A . A T . . G G A G G A A . A C C A G T G G C	Consensus #1
G C G T - A G A T A T G T G G A G G A A T A C C A G T G G C	Majority

685	G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	43030 16s
685	G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	genbank 16s 43030 AB059664
682	G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	49029 16s
682	G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	genbank 16s 49029 AB042059
666	G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	cc-4902516SRDNA-t7p_C02_006-1-ed
682	G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	genbank 16s 49025 AB042058
681	G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	Clostridium elmenteitii
700	G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	Geobacillus subterraneus 16S AF276307
683	G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	Sulfobacillus disulfidooxidans 16S U349
697	G C G T - A G A . A T G T G G A G G A A T A C C A G T G G C	Bacillus thermoleovorans ribosomal RNA

G A A G G C C C T T - G C T G G A C A G T G A C T G A C G	Consensus #1
. A A . G C G . C T . . . C T G G . C . G	Consensus #1
G A A G G C C C T T - G C T G G A C A G T G A C T G A C G	Majority

714	G A A R G C G C C T T - G C T G G A C A G T G A C T G A C G	43030 16s
714	G A A R G C G C C T T - G C T G G A C A G T G A C T G A C G	genbank 16s 43030 AB059664
711	G A A R G C G C C T T - G C T G G A C A G T G A C T G A C G	49029 16s
711	G A A R G C G C C T T - G C T G G A C A G T G A C T G A C G	genbank 16s 49029 AB042059
696	N A A R G C G C C T T - G C T G G A C A G T G A C T G A C G	cc-4902516SRDNA-t7p_C02_006-1-ed
711	G A A R G C G C C T T - G C T G G A C A G T G A C T G A C G	genbank 16s 49025 AB042058
710	G A A R G C G C C T T - G C T G G A C A G T G A C T G A C G	Clostridium elmenteitii
729	G A A R G C G C C T T - G C T G G A C A G T G A C T G A C G	Geobacillus subterraneus 16S AF276307
712	G A A R G C G C C T T - G C T G G A C A G T G A C T G A C G	Sulfobacillus disulfidooxidans 16S U349
726	G A A R G C G C C T T - G C T G G A C A G T G A C T G A C G	Bacillus thermoleovorans ribosomal RNA

Thursday, September 04, 2003 10:51 AM

C T G A G G C A C G A A A G C G T G G G A G C A A A C A G										Consensus #1
C T G A										Consensus #1
C T G A G G C A C G A A A G C G T G G G A G C A A A C A G										Majority
743	C	T	G	A	G	G	C	A	C	43030 16s
743	G	G	C	A	C	G	A	A	G	genbank 16s 43030 AB059664
740	G	T	G	A	G	G	C	A	A	49029 16s
740	G	G	C	A	C	G	A	A	G	genbank 16s 49029 AB042059
721	C	T	G	A	G	G	C	A	C	cc-4902516SRDNA-t7p_C02_006-1-ed
740	G	T	G	A	G	G	C	A	A	genbank 16s 49025 AB042058
739	G	T	G	A	G	G	C	A	A	Clostridium elmenteitii
758	G	T	G	A	G	G	C	A	A	Geobacillus subterraneus 16S AF276307
741	G	T	G	A	G	G	C	A	A	Sulfobacillus disulfidooxidans 16S U349
755	G	T	G	A	G	G	C	A	A	Bacillus thermoleovorans ribosomal RNA
G A T T A G A T A C C C T G G T A G T C C A C G C C G T A A										Consensus #1
.										Consensus #1
G A T T A G A T A C C C T G G T A G T C C A C G C C G T A A										Majority
773	G	A	T	T	A	G	A	T	A	43030 16s
773	G	A	T	T	A	G	A	T	A	genbank 16s 43030 AB059664
770	G	A	T	T	A	G	A	T	A	49029 16s
770	G	A	T	T	A	G	A	T	A	genbank 16s 49029 AB042059
725	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
770	G	A	T	T	A	G	A	T	A	genbank 16s 49025 AB042058
768	G	A	T	T	A	G	A	T	A	Clostridium elmenteitii
788	G	A	T	T	A	G	A	T	A	Geobacillus subterraneus 16S AF276307
771	G	A	T	T	A	G	A	T	A	Sulfobacillus disulfidooxidans 16S U349
784	G	A	T	T	A	G	A	T	A	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

A C G A T G A G T G C T A G G T G T T G G - G G G G T C A C																									Consensus #1
.																									Consensus #1
A C G A T G A G T G C T A G G T G T T G G - G G G G T C A C																									Majority

A	C	C	C	.	C	-	A	G	T	G	C	C	G	A	A	G	G	A	A	C	C	C	A	A	T	A	A	G	Consensus #1
.	Consensus #1
A	C	C	C	T	C	-	A	G	T	G	C	C	G	A	A	G	G	A	A	C	C	C	A	A	T	A	A	G	Majority

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Thursday, September 04, 2003 10:51 AM

	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	G	T	C	G	C	A	A	G	A	C	Consensus #1
	Consensus #1
	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	G	T	C	G	C	A	A	G	A	C	Majority
	910										920										930										
860	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	G	T	C	G	C	A	A	G	A	C	43030 16s
860	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	G	T	C	G	C	A	A	G	A	C	genbank 16s 43030 AB059664
858	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	G	T	C	G	C	A	A	G	A	C	49029 16s
858	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	G	T	C	G	C	A	A	G	A	C	genbank 16s 49029 AB042059
734	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
857	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	G	T	C	G	C	A	A	G	A	C	genbank 16s 49025 AB042058
854	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	C	T	C	G	C	A	A	G	A	C	Clostridium elmenteitii
878	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	G	C	C	G	C	A	A	G	A	C	Geobacillus subterraneus 16S AF276307
859	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	G	T	C	G	C	A	A	G	A	C	Sulfolobacillus disulfidooxidans 16S U349
873	C	A	C	T	C	C	G	C	C	T	G	G	G	G	A	G	T	A	C	G	G	C	C	G	C	A	A	G	A	C	Bacillus thermoleovorans ribosomal RNA

T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	-	C	C	C	G	Consensus #1
.	Consensus #1
T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	-	C	C	C	G	Majority

	940										950										960										
890	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	-	C	C	C	G	43030 16s
890	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	-	C	C	C	G	genbank 16s 43030 AB059664
888	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	-	C	C	C	G	49029 16s
888	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	-	C	C	C	G	genbank 16s 49029 AB042059
734	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
887	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	-	C	C	C	G	genbank 16s 49025 AB042058
884	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	A	C	C	C	G	Clostridium elmenteitii
908	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	-	C	C	C	G	Geobacillus subterraneus 16S AF276307
889	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	-	C	C	C	G	Sulfolobacillus disulfidooxidans 16S U349
903	T	G	A	A	A	C	T	C	A	A	A	G	G	A	A	T	T	G	A	C	G	G	G	G	G	-	C	C	C	G	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

C A C A G C A G T G G A G C A T G T G G T T T A A T T C G																									Consensus #1						
.																									Consensus #1						
C A C A G C A G T G G A G C A T G T G G T T T A A T T C G																									Majority						
919	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	T	T	A	A	T	T	C	G	43030 16s		
919	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	T	T	A	A	T	T	C	G	genbank 16s 43030 AB059664		
917	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	T	T	A	A	T	T	C	G	49029 16s		
917	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	T	T	A	A	T	T	C	G	genbank 16s 49029 AB042059		
734	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed			
916	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	genbank 16s 49025 AB042058	
914	C	A	C	A	A	G	C	A	G	C	G	C	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	Clostridium elmenteitii	
937	C	A	C	A	A	G	C	G	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	Geobacillus subterraneus 16S AF276307	
918	C	A	C	A	A	G	C	A	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	Sulfobacillus disulfidooxidans 16S U349	
932	C	A	C	A	A	G	C	G	T	G	G	A	G	C	A	T	G	T	G	G	T	T	A	A	T	T	C	G	Bacillus thermoleovorans ribosomal RNA		
A A G C A A C G C G A A G A A C C T T A C C A G G G C T T G																									Consensus #1						
. C . C G A A . A . C																									Consensus #1						
A A G C A A C G C G A A G A A C C T T A C C A G G G C T T G																									Majority						
949	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	43030 16s	
949	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	genbank 16s 43030 AB059664	
947	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	N	C	A	G	G	C	T	C	G	49029 16s	
947	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	genbank 16s 49029 AB042059	
734	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed			
946	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	genbank 16s 49025 AB042058	
944	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	T	G	A	G	C	T	T	G	Clostridium elmenteitii
967	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	T	C	T	T	G	Geobacillus subterraneus 16S AF276307
948	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	C	T	T	G	Sulfobacillus disulfidooxidans 16S U349	
962	A	A	G	C	A	A	C	G	C	G	A	A	G	A	A	C	C	T	T	A	C	C	A	G	G	T	C	T	T	G	Bacillus thermoleovorans ribosomal RNA

Alignment 2

Alignment Report of Ali 16S alignment.meg ClustalV (Weighted)

Thursday, September 04, 2003 10:51 AM

A C A T C C C . C T G A C A . C C . . A G A G A T - - G C										Consensus #1									
.										Consensus #1									
A C A T C C C T C T G A C A G C C G C A G A G A T - - G C										Majority									
1030										1040									
A C A T C C C T C T G A C A C C C T C A G A G A T - - G A										43030 16S									
979										genbank 16S 43030 AB059664									
A C A T C C C T C T G A C A C C C T C A G A G A T - - G A										49029 16S									
979										genbank 16S 49029 AB042059									
A C A T C C C T C T G A C A C C C T C A G A G A T - - G C										cc-4902516SRDNA-t7p_C02_006-1-ed									
744										genbank 16S 49025 AB042058									
A C A T C C C T C T G A C A C C C T C A G A G A T - - G T										Clostridium elmenteitii									
976										Geobacillus subterraneus 16S AF276307									
A C A T C C C T C T G A C A C C C T C A G A G A T - - G T										Sulfobacillus disulfidooxidans 16S U349									
974										Bacillus thermoleovorans ribosomal RNA									
A C A T C C C T C T G A C A C C C T C A G A G A T - - G T																			
A C A T C C C T C T G A C A C C C T C A G A G A T - - G T																			
997																			
A C A T C C C T C T G A C A C C C T C A G A G A T - - G T																			
978																			
A C A T C C C T C T G A C A C C C T C A G A G A T - - G T																			
992																			
G . . . T C C C T T C G G G G C A G - - . G G A G A C A G G										Consensus #1									
.										Consensus #1									
G G T T T C C C T T C G G G G C A G - - G G G A G A C A G G										Majority									
1060										1070									
G G G G T C C C T T C G G G G C A G - - A G G A G A C A G G										43030 16S									
1006										genbank 16S 43030 AB059664									
G G G G T C C C T T C G G G G C A G - - A G G A G A C A G G										49029 16S									
1006										genbank 16S 49029 AB042059									
G G T T T C C C T T C G G G G C A G - - G G G A G A C A G G										cc-4902516SRDNA-t7p_C02_006-1-ed									
1004										genbank 16S 49025 AB042058									
G G T T T C C C T T C G G G G C A G - - A G G A G A C A G G										Clostridium elmenteitii									
744										Geobacillus subterraneus 16S AF276307									
A C C T T C C C T T C G G G G C A G - - A G G A G A C A G G										Sulfobacillus disulfidooxidans 16S U349									
1003										Bacillus thermoleovorans ribosomal RNA									
A C C T T C C C T T C G G G G C A G - - A G G A G A C A G G																			
1001																			
A C C T T C C C T T C G G G G C A G - - A G G A G A C A G G																			
1026																			
G T C C C T T C G G G G C A G - - G G G A G A C A G G																			
1005																			
A C C G T C C C T T C G G G G C A G - - G G G A G A C A G G																			
1021																			
G T C C C T C - - - G G G G G A C A G G G T G A C A G G																			

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76307
6S U349
al RNA

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	1150										1160										1170										Consensus #1	Consensus #1	Majority	
	C	A	A	C	C	C	T	T	G	A	.	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	

	C	A	A	C	C	C	T	T	G	A	C	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	T	A
1094	C	A	A	C	C	C	T	T	G	A	C	C	T	G	T	G	T	T	A	C	C	A	G	C	G	C	G	T	T	G	43030	16s		
1094	C	A	A	C	C	C	T	T	G	A	C	C	T	G	T	G	T	T	A	C	C	A	G	C	G	C	G	T	T	G	genbank 16s	43030	AB059664	
1092	C	A	A	C	C	C	T	T	G	A	A	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	G	A	49029	16s		
1092	C	A	A	C	C	C	T	T	G	A	A	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	G	A	genbank 16s	49029	AB042059	
744	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed		
1091	C	A	A	C	C	C	T	T	G	A	T	C	T	G	T	G	T	T	A	C	C	A	G	C	A	C	G	T	A	G	genbank 16s	49025	AB042058	
1089	C	A	A	C	C	C	T	T	G	A	T	C	A	T	G	T	T	G	C	C	A	G	C	A	T	-	T	T	C	Clostridium elmenteitii				
1116	C	A	A	C	C	C	T	T	G	A	C	T	C	T	A	G	T	T	G	C	C	A	G	C	A	T	T	-	-	C	Geobacillus subterraneus 16S	AF276307		
1093	C	A	A	C	C	C	T	T	G	A	T	C	G	T	G	T	T	A	C	C	A	G	C	G	C	G	T	A	A	Sulfobacillus disulfidooxidans 16S	U349			
1107	C	A	A	C	C	C	T	T	G	A	C	T	C	T	C	T	A	G	T	T	G	C	C	A	G	C	A	C	G	-	A	Bacillus thermoleovorans ribosomal RNA		

A G G T G G G G A C T C A C A G G T G A C T G C C G G C G - Consensus #1
 G G G . A . Consensus #1
 A G G T G G G G A C T C A C A G G T G A C T G C C G G C G - Majority

	1180										1190										1200										
1124	A	G	G	C	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	43030 16S
1124	A	G	G	C	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	genbank 16S 43030 AB059664
1122	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	T	T	G	A	C	T	G	C	C	G	G	C	G	-	49029 16S
1122	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	T	T	G	A	C	T	G	C	C	G	G	C	G	-	genbank 16S 49029 AB042059
744	-	-	G	T	G	G	G	G	A	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
1121	A	G	G	T	G	G	G	G	A	C	T	C	A	C	A	G	G	T	G	A	C	T	G	C	C	G	G	C	G	-	genbank 16S 49025 AB042058
1118	G	G	A	T	G	G	G	C	A	C	T	C	T	A	A	T	G	A	G	A	C	T	G	C	C	G	G	T	G	A	Clostridium elmenteitii
1144	A	G	T	T	G	G	G	C	A	C	T	C	T	A	G	A	G	G	A	C	T	G	C	C	G	G	C	G	A	Geobacillus subterraneus 16S AF276307	
1123	A	G	G	C	G	G	G	G	A	C	T	C	A	C	A	C	G	T	G	A	C	T	G	C	C	G	T	C	G	-	Sulfobacillus disulfidooxidans 16S U349
1135	A	G	G	T	G	G	G	C	A	C	T	C	T	A	G	A	G	G	A	C	T	G	C	C	G	G	T	G	A	Bacillus thermoleovorans ribosomal RNA	

43030 16s
 genbank 16s 43030 AB059664
 49029 16s
 genbank 16s 49029 AB042059
 cc-4902516SRDNA-t7p_C02_006-1-ed
 genbank 16s 49025 AB042058
 Clostridium elmentei
 Geobacillus subterraneus 16S AF276307
 Sulfolobacillus disulfidooxidans 16S U349
 Bacillus thermoleovorans ribosomal RNA

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T A A G T C G G A G G A A G G C G G G G A T G A C G T C A A										Consensus #1
.										Consensus #1
T A A G T C G G A G G A A G G C G G G G A T G A C G T C A A										Majority
1153	T	A	A	G	T	C	G	G	A	43030 16s
1153	T	A	A	G	T	C	G	G	A	genbank 16s 43030 AB059664
1151	T	A	A	G	T	C	G	G	A	49029 16s
1151	T	A	A	G	T	C	G	G	A	genbank 16s 49029 AB042059
752	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
1150	T	A	A	G	T	C	G	G	A	genbank 16s 49025 AB042058
1148	C	A	A	C	G	G	A	A	G	Clostridium elmenteitii
1174	A	A	G	T	C	G	G	A	A	Geobacillus subterraneus 16S AF276307
1152	T	A	A	G	A	C	G	G	A	Sulfobacillus disulfidooxidans 16S U349
1165	C	A	A	G	T	C	G	G	A	Bacillus thermoleovorans ribosomal RNA
A T C A T C A T G C C C C T T A T G T C C T G G G C T A C A										Consensus #1
.										Consensus #1
A T C A T C A T G C C C C T T A T G T C C C T G G G C T A C A										Majority
1183	A	T	C	A	T	C	A	T	G	43030 16s
1183	A	T	C	A	T	C	A	T	G	genbank 16s 43030 AB059664
1181	A	T	C	A	T	C	A	T	G	49029 16s
1181	A	T	C	A	T	C	A	T	G	genbank 16s 49029 AB042059
752	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
1180	A	T	C	A	T	C	A	T	G	genbank 16s 49025 AB042058
1178	A	T	C	A	T	C	A	T	G	Clostridium elmenteitii
1204	A	T	C	A	T	C	A	T	G	Geobacillus subterraneus 16S AF276307
1182	A	T	C	A	T	C	A	T	G	Sulfobacillus disulfidooxidans 16S U349
1195	A	T	C	A	T	C	A	T	G	Bacillus thermoleovorans ribosomal RNA

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	1270										1280										1290										Consensus #1	Consensus #1	Majority					
	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	.	G	G	G	A	.	G	G	A	.	G	G	A	

	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	C	G	G	G	A	A	C	G	G	G	A	A	A	
1213	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	C	A	A	A	G	G	G	A	G	G	G	A	G	G	A	G	43030 16s
1213	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	A	C	A	A	A	G	G	G	A	G	G	G	A	G	G	A	genbank 16s 43030 AB059664	
1211	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	C	G	G	G	A	A	C	G	G	A	A	A	49029 16s	
1211	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	C	G	G	G	A	A	C	G	G	A	A	A	genbank 16s 49029 AB042059	
752	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed		
1210	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	C	G	G	G	A	A	C	G	G	A	A	A	genbank 16s 49025 AB042058	
1208	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	A	T	A	C	A	A	A	G	G	G	C	A	G	G	C	A	A	Clostridium elmenteitii	
1234	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	A	G	G	G	C	T	G	G	C	T	G	A	Geobacillus subterraneus 16S AF276307	
1212	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	C	A	C	A	A	C	G	G	G	A	C	G	G	A	C	A	C	Sulfobacillus disulfidooxidans 16S U349	
1225	C	A	C	G	T	G	C	T	A	C	A	A	T	G	G	G	C	G	G	T	A	C	A	A	A	G	G	G	C	T	G	G	C	T	G	A	Bacillus thermoleovorans ribosomal RNA	

G	C	G	A	A	.	C	C	G	C	G	A	G	G	.	G	G	A	G	C	.	A	A	.	C	C	C	A	.	A								Consensus #1
.	Consensus #1
G	C	G	A	A	G	C	C	G	C	G	A	G	G	T	G	G	A	G	C	G	A	A	C	C	C	C	A	A	A	A	A	A	A	A	A	Majority	

	1300										1310										1320										
1243	G	C	G	A	A	G	C	C	G	C	G	A	G	G	C	G	A	G	C	G	A	A	A	C	C	C	A	A	A	43030 16S	
1243	G	C	G	A	A	G	C	C	G	C	G	A	G	G	C	G	A	G	C	G	A	A	A	C	C	C	A	A	A	genbank 16S 43030 AB059664	
1241	G	C	G	A	G	A	C	C	G	C	G	A	G	G	T	G	G	A	G	C	A	A	A	C	C	C	T	G	A	49029 16S	
1241	G	C	G	A	G	A	C	C	G	C	G	A	G	G	T	G	G	A	G	C	A	A	A	C	C	C	T	G	A	genbank 16S 49029 AB042059	
760	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed	
1240	G	C	G	A	A	G	C	C	G	C	G	A	G	G	T	G	G	A	G	C	A	A	A	C	C	T	A	A	A	genbank 16S 49025 AB042058	
1238	G	C	G	A	A	G	A	C	C	G	C	A	T	C	C	G	G	A	G	C	A	A	C	C	C	C	A	T	A	Clostridium elmenteitii	
1264	G	C	G	A	A	C	C	C	G	C	G	A	G	G	G	G	A	G	C	G	A	A	T	C	C	C	C	A	A	Geobacillus subterraneus 16S AF276307	
1242	G	C	G	A	G	A	C	C	G	C	A	A	T	C	T	G	G	A	G	C	A	A	C	C	C	C	T	G	A	Sulfobacillus disulfidooxidans 16S U349	
1255	G	C	G	A	A	C	C	C	G	C	G	A	G	G	G	G	A	G	C	G	A	A	T	C	C	C	C	A	A	Bacillus thermoleovorans ribosomal RNA	

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A A G C C G . T C G T A G T T C G G A T T G C A G G C T G C										Consensus #1
. T T										Consensus #1
A A G C C G C T C G T A G T T C G G A T T G C A G G C T G C										Majority
A A G C C G C T C G T A G T T C G G A T T G C A G G C T G C										43030 16S
A A G C C G C T C G T A G T T C G G A T T G C A G G C T G C										genbank 16S 43030 AB059664
A A G C C G C T C G T A G T T C G G A T T G C A G G C T G C										49029 16S
A A G C C G C T C G T A G T T C G G A T T G C A G G C T G C										genbank 16S 49029 AB042059
- - - - - T T A N A - - - - -										cc-4902516SRDNA-t7p_C02_006-1-ed
A A G C C G C T C G T A G T T C G G A T T G C A G G C T G C										genbank 16S 49025 AB042058
A A G T C G G T C C C A G T T C C G G A T T G A G G C T G C										Clostridium elmenteitii
A A G C C G C T C C C A G T T C C G G A T T G C A G G C T G C										Geobacillus subterraneus 16S AF276307
A A G C C G C T C C C A G T T C C G G A T T G C A G G C T G C										Sulfobacillus disulfidooxidans 16S U349
A A G C C G C T C C C A G T T C C G G A T T G C A G G C T G C										Bacillus thermoleovorans ribosomal RNA
A A C T C G C C T G C A T G A A G C C G G A A T T G C T A G										Consensus #1
.										Consensus #1
A A C T C G C C T G C A T G A A G C C G G A A T T G C T A G										Majority
A A C T C G C C T G C A T G A A G C C G G A A T T G C T A G										43030 16S
A A C T C G C C T G C A T G A A G C C G G A A T T G C T A G										genbank 16S 43030 AB059664
A A C T C G C C T G C A T G A A G C C G G A A T T G C T A G										49029 16S
A A C T C G C C T G C A T G A A G C C G G A A T T G C T A G										genbank 16S 49029 AB042059
- - - - -										cc-4902516SRDNA-t7p_C02_006-1-ed
A A C T C G C C T G C A T G A A G C C G G A A T T G C T A G										genbank 16S 49025 AB042058
A A C T C G C C C C C A T G A A G T T G G A T T G C T A G										Clostridium elmenteitii
A A C T C G C C C C C A T G A A G C C G G A A T T G C T A G										Geobacillus subterraneus 16S AF276307
A A C T C G C C C C C A T G A A G C C G G A A T T G C T A G										Sulfobacillus disulfidooxidans 16S U349
A A C T C G C C C C C A T G A A G C C G G A A T T G C T A G										Bacillus thermoleovorans ribosomal RNA

Alignment 2

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T A A T C G C G G A T C A G C A T G C C G C G G T G A A T .																										Consensus #1					
.																										Consensus #1					
T A A T C G C G G A T C A G C A T G C C G C G G T G A A T C																										Majority					
1390													1400													1410					
1333	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	43030 16s
1333	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	genbank 16s 43030 AB059664
1331	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	49029 16s
1331	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	genbank 16s 49029 AB042059
765	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	cc-4902516SRDNA-t7p_C02_006-1-ed
1330	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	genbank 16s 49025 AB042058
1328	T	A	A	T	C	G	C	G	A	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	G	Clostridium elmenteitii
1354	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	Geobacillus subterraneus 16S AF276307
1332	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	C	Sulfobacillus disulfidooxidans 16S U349
1345	T	A	A	T	C	G	C	G	G	A	T	C	A	G	C	A	T	G	C	C	G	C	G	G	T	G	A	A	T	A	Bacillus thermoleovorans ribosomal RNA
C G T T C C C G G G C C C T T G T A C A C A C C G C C C G T C																										Consensus #1					
. . T . C C C																										Consensus #1					
C G T T C C C G G G C C C T T G T A C A C A C C G C C C G T C																										Majority					
1420													1430													1440					
1363	C	G	T	T	C	C	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	43030 16s				
1363	C	G	T	T	C	C	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	genbank 16s 43030 AB059664				
1361	C	G	T	T	C	C	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	49029 16s				
1361	C	G	T	T	C	C	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	genbank 16s 49029 AB042059				
765	-	-	T	C	C	C	C	C	N																					cc-4902516SRDNA-t7p_C02_006-1-ed	
1360	C	G	T	T	C	C	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	genbank 16s 49025 AB042058				
1358	C	G	T	T	C	C	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	Clostridium elmenteitii				
1384	C	G	T	T	C	C	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	Geobacillus subterraneus 16S AF276307				
1362	C	G	T	T	C	C	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	Sulfobacillus disulfidooxidans 16S U349				
1375	C	G	T	T	C	C	C	C	T	T	G	T	A	C	A	C	A	C	C	G	C	C	C	G	T	C	Bacillus thermoleovorans ribosomal RNA				

Alignment 2

A C A C C A C G A G A G T C G G C A A C A C C C G A A G T C													Consensus #1																			
.													Consensus #1																			
A C A C C A C G A G A G T C G G C A A C A C C C G A A G T C													Majority																			
1450													1470																			
A C A C C A C G A G A G T C G G C A A C A C C C G A A G T C													43030 16s																			
1393	A	C	A	C	C	A	C	G	A	G	A	G	T	C	genbank 16s 43030 AB059664																	
1393	A	C	A	C	C	A	C	G	A	G	A	G	A	G	T	C	49029 16s															
1391	A	C	A	C	C	A	C	G	A	G	A	G	A	G	A	G	T	C	genbank 16s 49029 AB042059													
1391	A	C	A	C	C	A	C	G	A	G	A	G	A	G	A	G	A	G	T	C	cc-4902516SRDNA-t7p_C02_006-1-ed											
770																genbank 16s 49025 AB042058																
1390	A	C	A	C	C	A	C	G	A	G	A	G	A	G	A	G	A	G	T	C	Clostridium elmenteitii											
1388	A	C	A	C	C	A	C	G	A	G	A	G	A	G	A	G	A	G	T	C	Geobacillus subterraneus 16S AF276307											
1414	A	C	A	C	C	A	C	G	A	G	A	G	A	G	A	G	A	G	T	C	Sulfobacillus disulfidooxidans 16S U349											
1392	A	C	A	C	C	A	C	G	A	G	A	G	A	G	A	G	A	G	T	C	Bacillus thermoleovorans ribosomal RNA											
1405	A	C	A	C	C	A	C	G	A	G	A	G	A	G	A	G	A	G	T	C												
G G T G . G G T A A C C C . T . . . G G G . G C C A G C C G													Consensus #1																			
.													Consensus #1																			
G G T G A G G T A A C C C G T G T A G G G A G C C A G C C G													Majority																			
1480													1490	1500																		
G G T G A G G T A A C C C C T G T G G G A G C C A G C C G													43030 16s																			
1423	G	G	T	G	A	G	G	T	A	A	C	C	C	T	G	T	G	G	A	G	C	C	C	G	genbank 16s 43030 AB059664							
1423	G	G	T	G	A	G	G	T	A	A	C	C	C	C	T	G	T	G	G	A	G	C	C	A	G	C	C	G	49029 16s			
1421	G	G	T	G	A	G	G	T	A	A	C	C	C	C	T	G	T	G	A	G	C	C	A	G	C	C	C	G	genbank 16s 49029 AB042059			
1421	G	G	T	G	A	G	G	T	A	A	C	C	C	C	T	G	T	G	A	G	C	C	A	G	C	C	C	G	cc-4902516SRDNA-t7p_C02_006-1-ed			
770																genbank 16s 49025 AB042058																
1420	G	G	T	G	A	G	G	T	A	A	C	C	C	-	G	T	-	T	A	T	G	G	A	G	C	C	A	G	C	C	C	Clostridium elmenteitii
1418	C	G	T	T	A	C	C	G	A	A	C	C	C	T	T	C	G	G	A	C	G	G	-	-	A	A	C	G	G	Geobacillus subterraneus 16S AF276307		
1444	G	G	T	G	A	G	G	T	A	A	C	C	C	T	T	A	C	-	G	G	G	A	G	C	C	A	G	C	C	C	Sulfobacillus disulfidooxidans 16S U349	
1422	G	G	T	G	A	G	G	T	A	A	C	C	C	T	A	-	A	G	G	G	G	G	C	C	A	G	C	C	C	G	Bacillus thermoleovorans ribosomal RNA	
1428																																

Thursday, September 04, 2003 10:51 AM

	C	C	G	A	A	G	G	T	G	G	G	.	.	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G	Consensus #1									
	Consensus #1									
	C	C	G	A	A	G	G	T	G	G	G	T	C	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G	Majority									
	1510														1520														1530									
1453	C	C	G	A	A	G	G	T	G	G	G	G	T	C	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G	43030 16s								
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1450	C	C	G	A	A	G	G	T	G	G	G	G	T	T	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G	49029 16s								
1450	C	C	G	A	A	G	G	T	G	G	G	G	T	T	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G	genbank 16s 49029 AB042059								
770	cc-4902516SRDNA-t7p_C02_006-1-ed																																					
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1445	T	C	G	A	A	G	G	T	G	A	A	G	C	C	G	A	T	A	C	T	G	G	G	T	G	A	A	G	Clostridium elmenteitii									
1473	C	C	G	A	A	G	G	T	G	G	G	G	C	A	A	G	T	G	A	T	T	G	G	G	T	G	A	A	G	Geobacillus subterraneus 16S AF276307								
1451	C	C	G	A	A	G	G	T	G	G	G	G	C	C	G	A	T	G	A	T	T	G	G	G	T	G	A	A	G	Sulfobacillus disulfidooxidans 16S U349								
1428	Bacillus thermoleovorans ribosomal RNA																																					
	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	Consensus #1									
	Consensus #1									
	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	X	X	X	X	X	X	X	X	X	X	Majority									
	1540														1550														1560									
1483	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T															43030 16s					
1483	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	A	C	C	G	G	A	A	G	G	T	G	C	genbank 16s 43030 AB059664							
1480	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T															49029 16s					
1480	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	A	T	C	G	G	A	A	G	G	T	G	C	genbank 16s 49029 AB042059							
770	cc-4902516SRDNA-t7p_C02_006-1-ed																																					
1478	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	A	T	C	G	G	A	A	G	G	T	G	C	genbank 16s 49025 AB042058							
1475	T	C	G	T	A	A	C	A	A	G	G	T	A	T	C	C	G	T															Clostridium elmenteitii					
1503	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T	A	C	C	G	G	A	A	G	G	T	G	C	Geobacillus subterraneus 16S AF276307							
1481	T	C	G	T	A	A	C	A	A	G	G	T	A	G	C	C	G	T															Sulfobacillus disulfidooxidans 16S U349					
1428	Bacillus thermoleovorans ribosomal RNA																																					

Alignment 2

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.
X X X X X X X X X X X X X X X

Consensus #1
Consensus #1
Majority

1570

1500

1513 G G T T G G A T

1497

1510 G G T T G G A T

770

1508 G G T T G G A

1492

1533 G G C T G G A T C A C C T C C T

1496

1428

43030 16S

genbank 16S 43030 AB059664

49029 16S

genbank 16S 49029 AB042059

cc-4902516SRDNA-t7p_C02_006-1-ed

genbank 16S 49025 AB042058

Clostridium elmenteitii

Geobacillus subterraneus 16S AF276307

Sulfolobus solfataricus 16S U349

Bacillus thermoleovorans ribosomal RNA

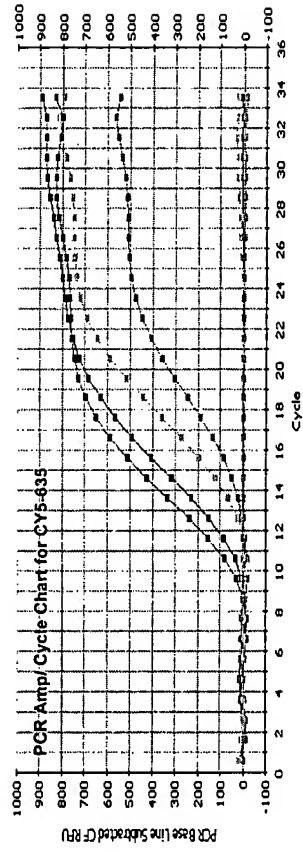
Consensus 'Consensus #1': When 60% (6) match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Shade (with black at 40% fill) residues that match the consensus named 'Consensus #1' exactly.

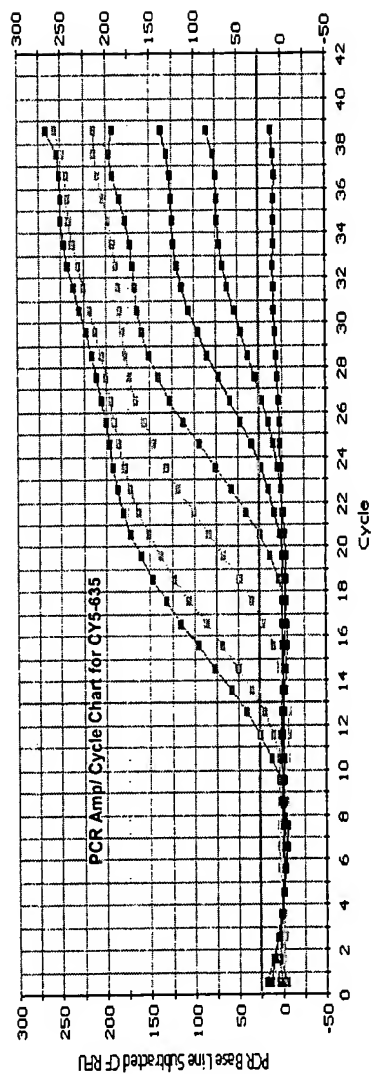
Decoration 'Decoration #1': Box residues that match the Consensus exactly.

Figure 9

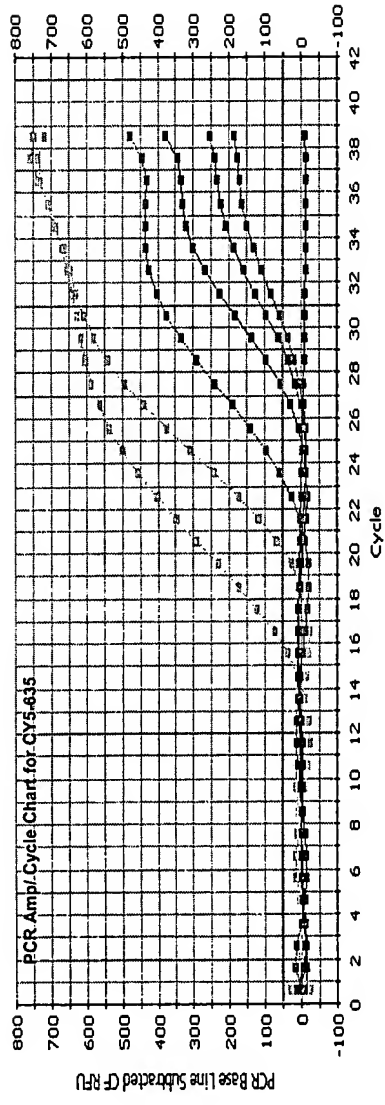


In addition, *G. stearothermophilus* can be seen in green. Other curves below the base line include the blank control (red) and the tests for *Lactococcus lactis* C2 (blue), *P. putida* 49L/51 (purple) and *E. coli* DH5α (orange) using the same primer and probe set.

Figure 10



. Dilutions 10^0 (red), 10^{-1} (orange), 10^{-2} (lt. blue), 10^{-3} (purple), 10^{-4} (black), and 10^{-5} (blue) can be seen above the baseline. The blank control (brown) is below the baseline.



Dilutions 10⁻¹ (orange), 10⁻² (light blue), 10⁻³ (purple), 10⁻⁴ (black), 10⁻⁵ (blue), 10⁻⁶ (green) can be seen above the baseline. The blank control (red) is below the baseline.

Figure 11

Figure 12

Zygosaccaromyces
 5 ATTGGGCCCTCTANAGCATGCTCGACGGCCGCCAGTGTGATGGATATCTGCAGAAATTCGGCTTTGCATGGCCGTTCTTAG
 TTGGTGGAGTGATTTGTCTGTCTTAATTGCCGATAACGAACGAGACCTTAACCTACTAAATAGTGGTGTAGCATTTGCTGG
 TTTTTCACNTTCTTAGAGGGACTATCGGTTTCAAGCCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTAGA
 CGTTCGGGCCGCACGGCGCTACACTGACGGAGCCAGCGAGTCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAA
 CTCGTCTGTGGGATAGAGCATTTGTAATTATTGCTCTTCAACGAGGAATTCCCTAGTAAGCGCAAGTCATCAACTTGC
 GTTGATTACGTCCCTGCCCTTTGTACACAAAGCCGAATTCAGCACACTGGCGGCCGTTACTAGTGGATCCGAGCTCGG
 TACCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCTGTGTGAAAATTGTTATCCGCTCACAAATCCACACAACATACGA
 GCCGGAAGCATAAAGTGTAAGCCGTGGGTGCCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGC
 TTTCAGTCGGGAAACCTGTCTGTGCCAGCTGCATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTGCGTATTGGGC
 GCTCTTCCGCTTCCCTCGCTCACTGACTCGCTCGGTCGGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGCGG
 GTAAACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCANANGCCAGGANCCTGT
 10 AAAAGCCGCGTGGCGTTTTCNCNTANGCTCGCCCCCTGACAGCATNCAAAATCGACGCTCAGTCNNANGTGGCGAAC
 CCGNNGGANATAAGATACNNGCGTTNCCCCGTGNANCTCCNCNTGGCTNTCNGTNCNANCNGNCNGTANGGAANCTGNCNC
 CTTTCNCCTTNGGAACNGGNNCTTNNNNNNNANCNNGNNNNNNNNNNNGGNNN

Figure 13

Penicillium digitatum

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5  GANGNCNNCCNNANTNNATCCTNAGCNGAGTGNNAAGCCNCGTTNCCGANGGAGAAGNGGACAGGTNTCCGTANCGC
   AGGTNNGANCAAGAGAGCGCACGAGGGAGCTNCAGGGGAAACGCCCTGGGATCTTNATAGTCCNGTCGGGTTTCNCCACNT
   CTGACTTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCNTATGGAAAACGCCAGCAACCGGGCCCTTTTACGGTT
   CCTGGCNTTTGTGGCCCTTTTGTCTACATGTTCTTCCCTGCCGTTATCCCCCTGATTCTGTGGATAACCGTATTACCGCCTT
   TGAGTGAGCTGATACCGCTCGCCGAGCCGAAACGACCGAGCGAGTCAGTGAGCGGAGGAAAGCGGCCCAA
   10  TACGCAAAACCGCCTCTCCCCGCGGTTGGCCGATTCAATTAATGCAGCTGGCACGACAGGTTTCCCAGACTGGAAGCGGGC
   AGTGAGCGCAACGCAATTAAATGTGAGTTAGCTCACTCATTAGGCACCCAGGCTTACACTTTATGCTTCCGGCTCGTAT
   GTTGTGTGGAAATTGTGAGCGGATAACAAATTTCAACAGGAAACAGCTATGACCATGATTACGCCAAAGCTTGGTACCGAGC
   TCGGATCCACTAGTAACGGCCGCGAGTGTGTGGAATTTCGGCTTTGCATGGCCGTTCTTAGTTGGTGAGTGATTGTCT
   GCTTAATTGCGATAACGAACGAGACCTCGGCCCTTAAATAGCCCGTCCGCATTTGCGGGCCGCTGGCTTCTTAAGGGGA
   15  CTATCGGCTCAAGCCGATGGAAAGTGCGCGGCAATAACAGGTCTGTGATGCCCTTAGATGTTCTGGGCCGACGCGCGCTA
   CACTGACAGGGCCAGCGAGTACATCACCTTAACCGAGAGGTTTGGGTAATCTTGTAAACCTGTCTGTGGGATAGA
   GCATTGCAATTATTGCTCTTCAACGAGGAATGCC'TAGTAGGCACGAGTCAATCAGCTCGTGCCGATTACGTCCCTGCCCCTT
   TGTAACACAAAGCCGAAATTCTGCAGATAATCCATCACACTGGCGGCCGTCGAGCATGCTNTAGAGGGCCCAAT
```

5

10

15

20

Figure 15

PCR Amp/Cycle Graph for FAM-490

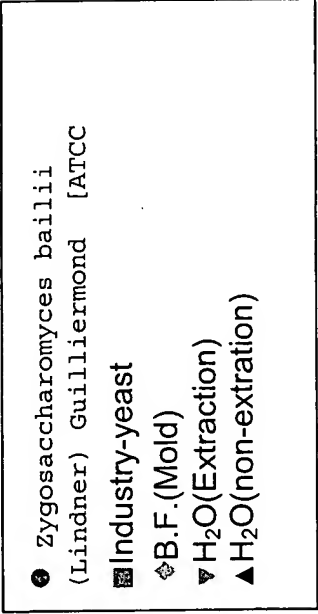
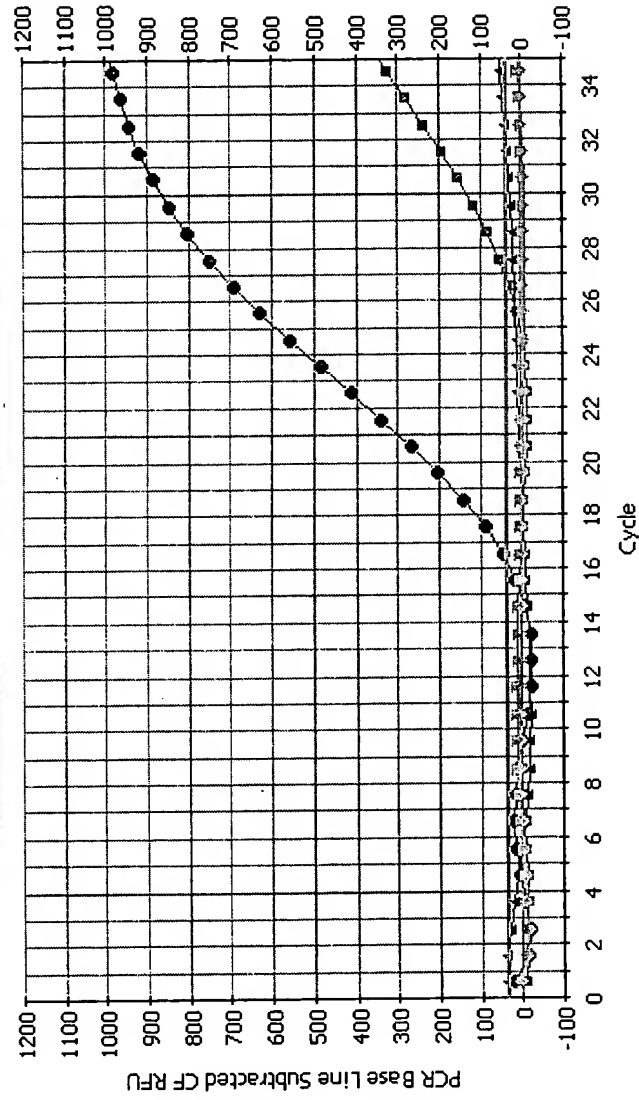


Figure 16

PCR Amp/Cycle Graph for FAM-490

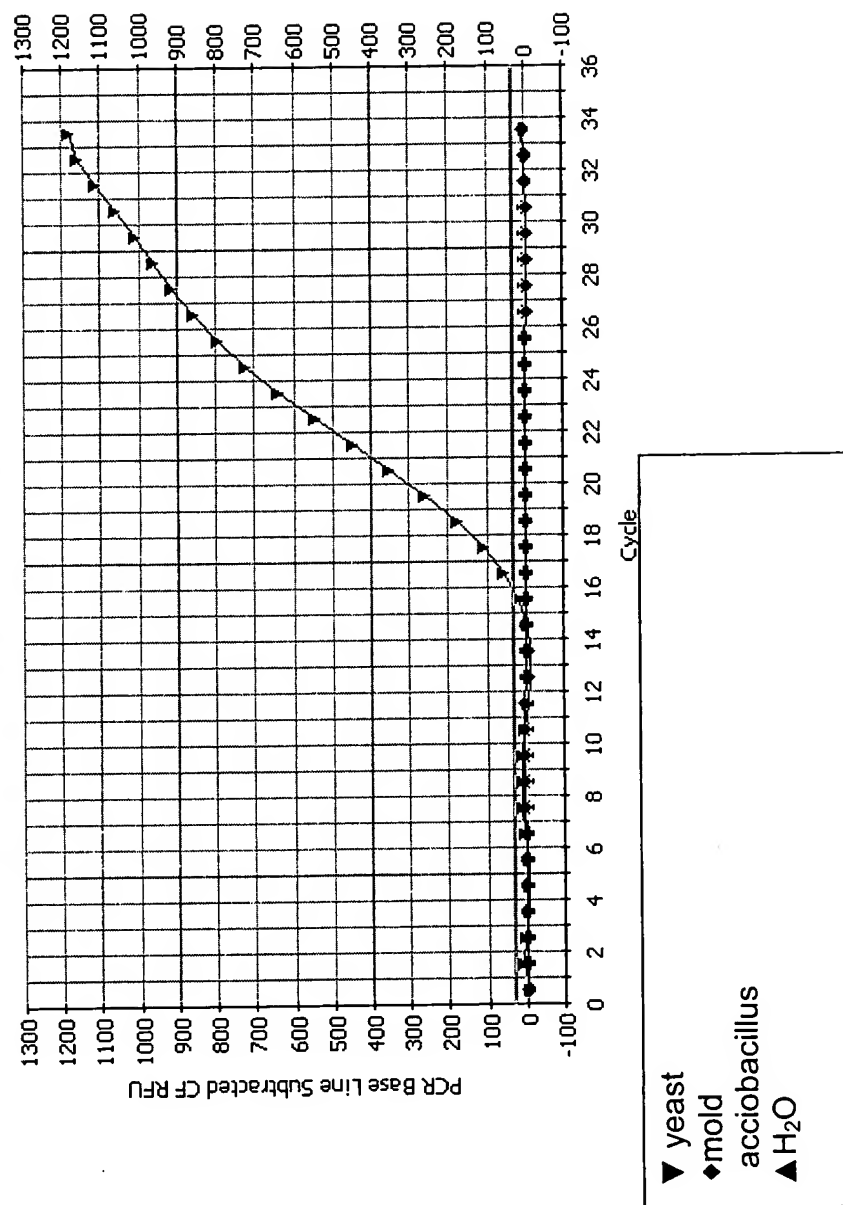


Figure 17

PCR Amp/Cycle Graph for FAM-490

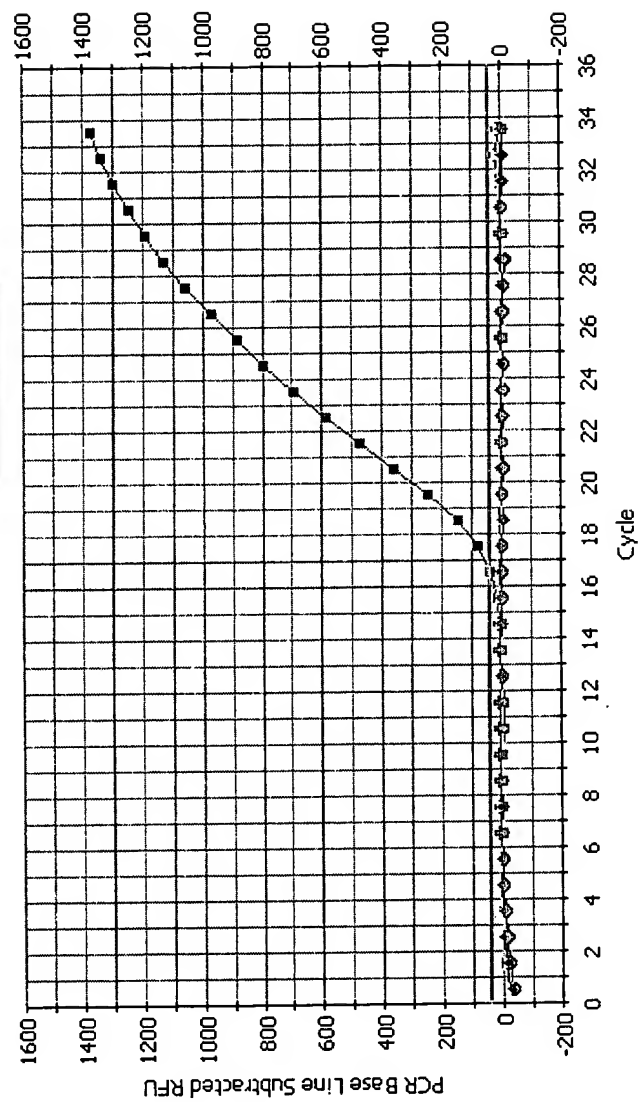


Figure 18

PCR Amp/Cycle Graph for FAM-490

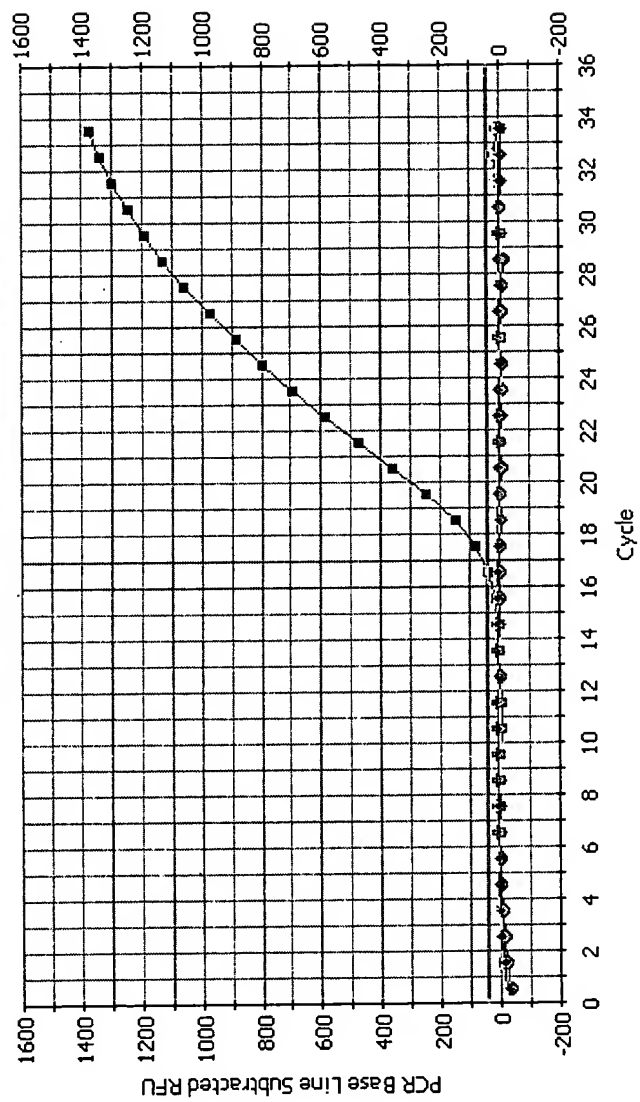
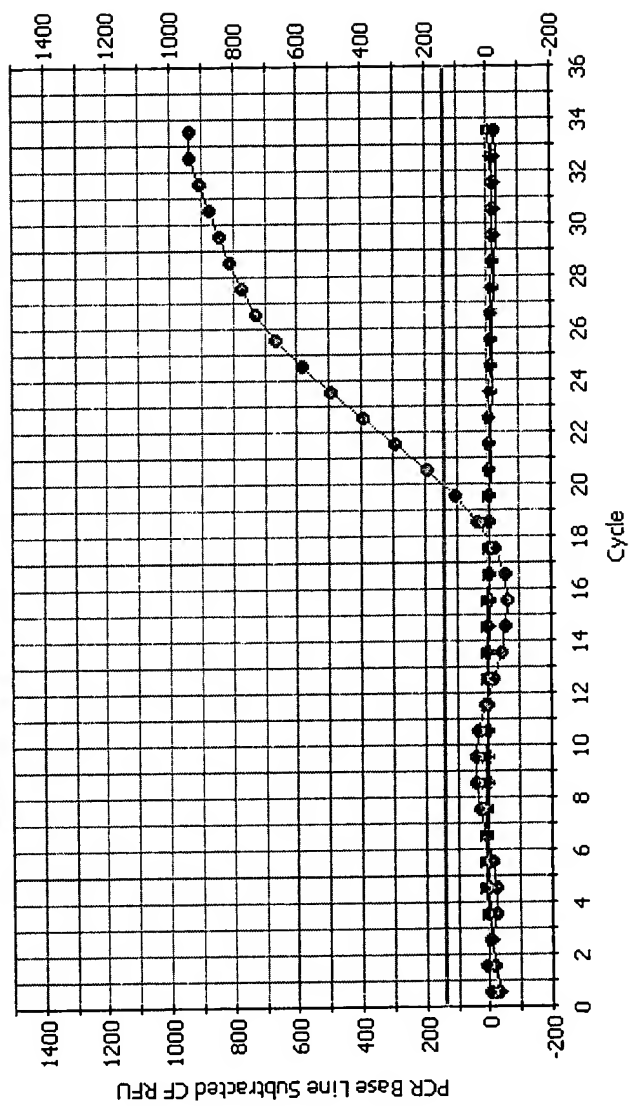


Figure 19

PCR Amp/Cycle Graph for FAM-490



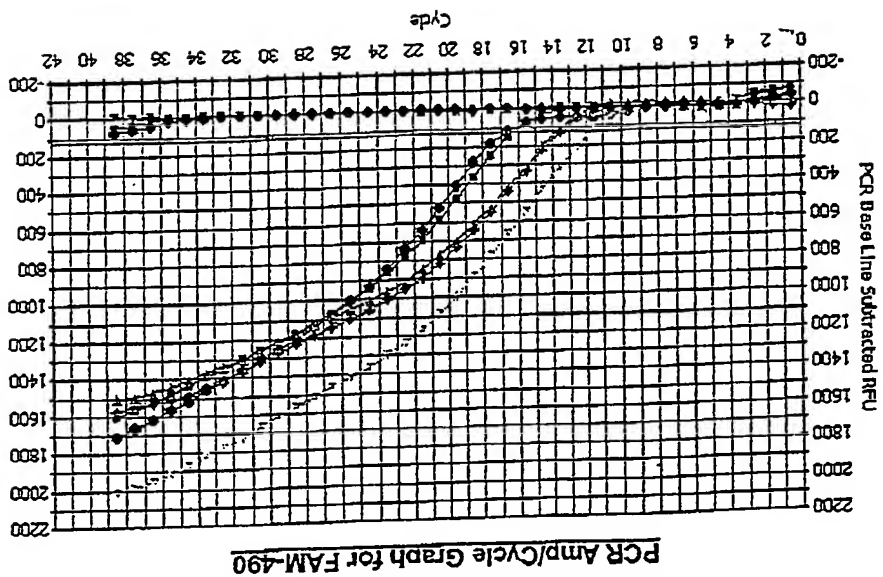


Figure 20

Figure 21

PCR Amp/Cycle Graph for FAM-490

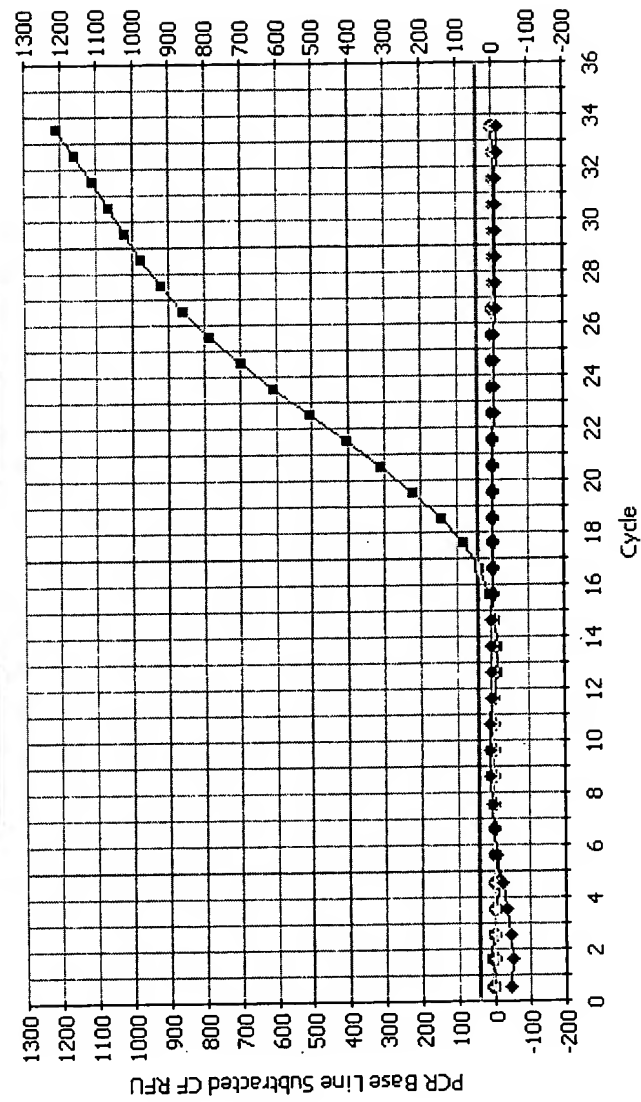


Figure 22

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1  CGTAGTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
2  CGTAGTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
3  CGTAGTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
4  CGTAGTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
5  CGTAGTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
6  CGTAGTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
7  CCCAGTTCGGATTGAGGGCTGCAACTCGCCCCCATGAAGT
8  CTCAGTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
9  CGTAGTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC
10 CTCAGTTCGGATTGCAGGCTTGCAACTCGCCTGCATGAAGC

1  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTT
2  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTT
3  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTT
4  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTT
5  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTT
6  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTT
7  TGGAGTTGCTAGTAATCGCGAATCAGCATGTCGCGGTGAATGCGTTT
8  CGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTT
9  CGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATCCGTTT
10 CGGAATCGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTT

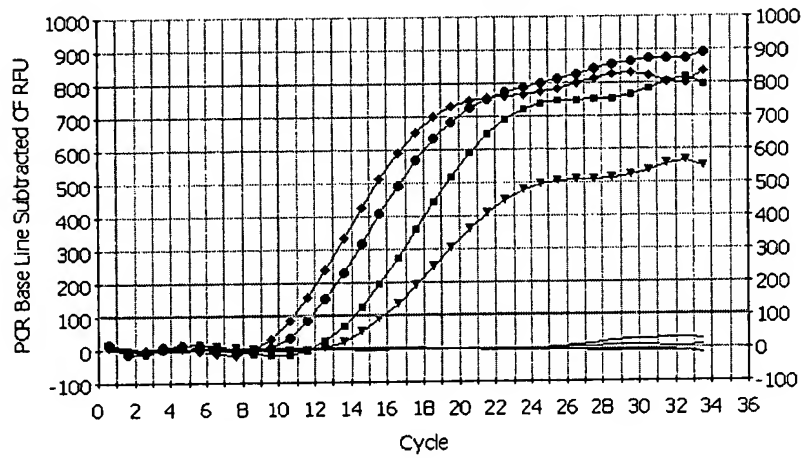
1  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
2  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
3  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
4  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
5  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
6  CCGGGCCTTGTACACACCGCCCGTCACACACACGAGAGTTCGGCAACAC
7  CCGGGTCTTGTACACACCGCCCGTCACACACCGGAAGTTCGGAAGCAC
8  CCGGGCCTTGTACACACCGCCCGTCACACACGAGAGCTTGCAACAC
9  CCGGGCCTTGTACACACCGCCCGTCACACACGAGAGTTCGCAACAC
10 CCGGGCCTTGTACACACCGCCCGTCACACACGAGAGCTCGCAACAC

```

^a 16S rDNA Sequences in the alignment are 16S rDNA sequences from the following organisms (GenBank accession numbers follow if applicable): 1) *A. acidocaldarius* strain ATCC 43030, 2) *A. acidocaldarius* strain DSM 454 (AB059664), 3) *A. cycloheptanicus* strain ATCC 49029, 4) *A. cycloheptanicus* strain DSM 4006 (AB042059), 5) *A. acidoterrestris* strain ATCC 49025, 6) *A. acidoterrestris* strain DSM 3923 (AB042058), 7) *Clostridium elmenteitii* isolate E2SE1-B (AJ271453), 8) *Geobacillus subterraneus* strain K (AF276307), 9) *Sulfobacillus disulfidooxidans* SD-11 (U34974), and 10) *B. thermoleovorans* strain ATCC 43513 (M77488) ^b

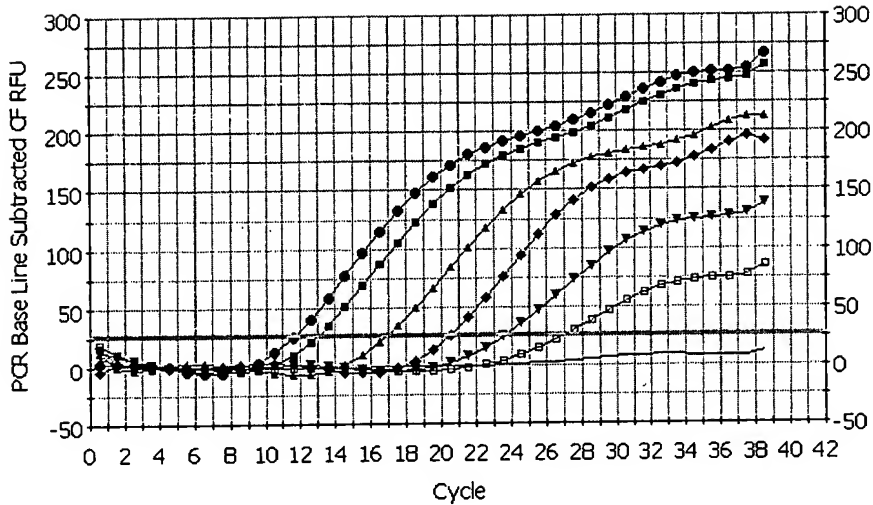
Note CC16S-R is in 5' to 3' orientation in alignment. Actual primer sequence is the reverse complement.

Figure 23



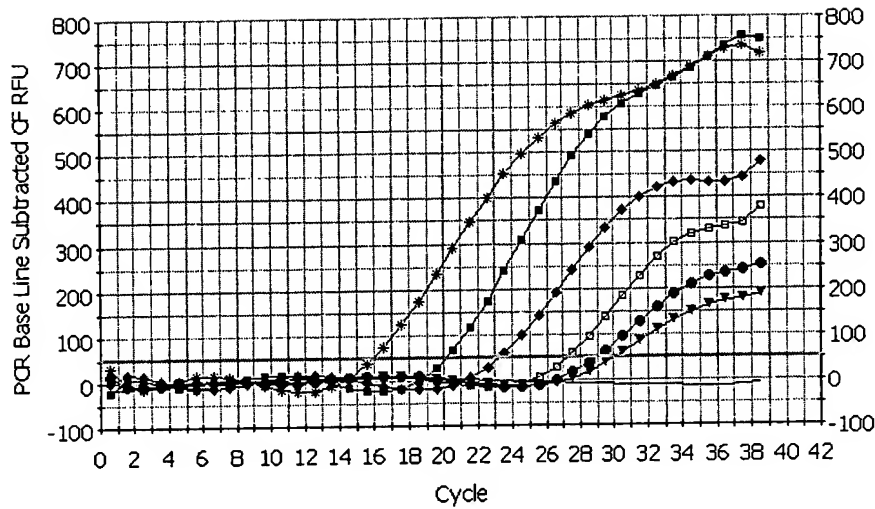
In addition, *G. stearo**thermophilus* ATCC 10149 (▼) can be detected. Curves below the base
5 line include the blank control, *Lactococcus lactis* C2, *P. putida* 49L/51, and *E. coli* DH5 α . This
is a representative curve of repeated trials.

Figure 24



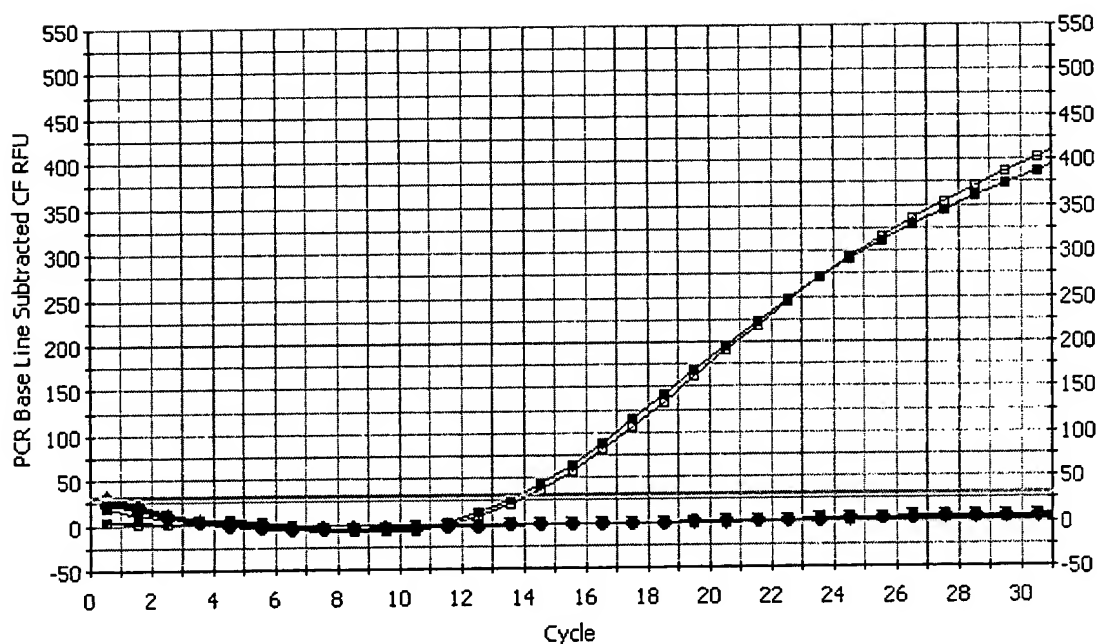
. Ten-fold serial dilutions were performed, and cell numbers^a represented at each curve are as follows: 1.6x10⁷ CFU/ml (●), 1.6x10⁶ CFU/ml (■), 1.6x10⁵ CFU/ml (▲), 1.6x10⁴ CFU/ml (◆), 1.6x10³ CFU/ml (▼), and 1.6x10² CFU/ml (□) appear above the baseline. The water control is below the baseline. This is a representative curve of repeated trials. ^a Cell numbers were calculated by finding the CFU/ml of plated samples and multiplying by the dilution level of the representative curve.

Figure 25



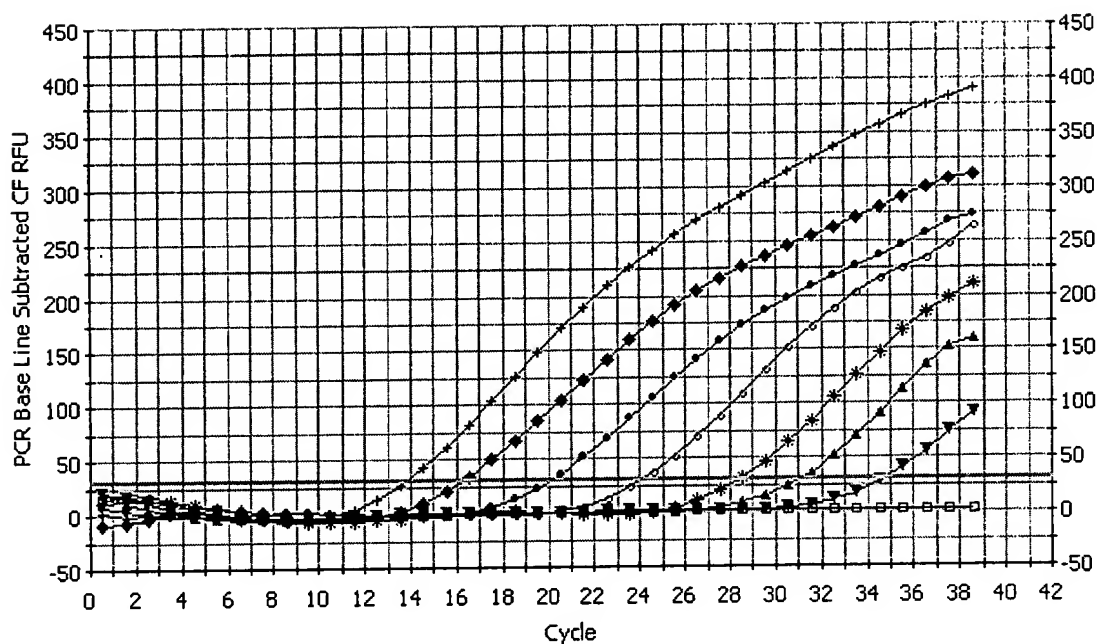
- 5 Cell counts at each curve are as follows: 6.3×10^6 CFU/ml (+), 6.3×10^5 CFU/ml (■), 6.3×10^4 CFU/ml (◆), 6.3×10^3 CFU/ml (□), 6.3×10^2 CFU/ml (●), and 6.3×10^1 CFU/ml (▼) appear above the baseline. The water control is below the baseline. This is a representative curve of repeated trials.

Figure 26



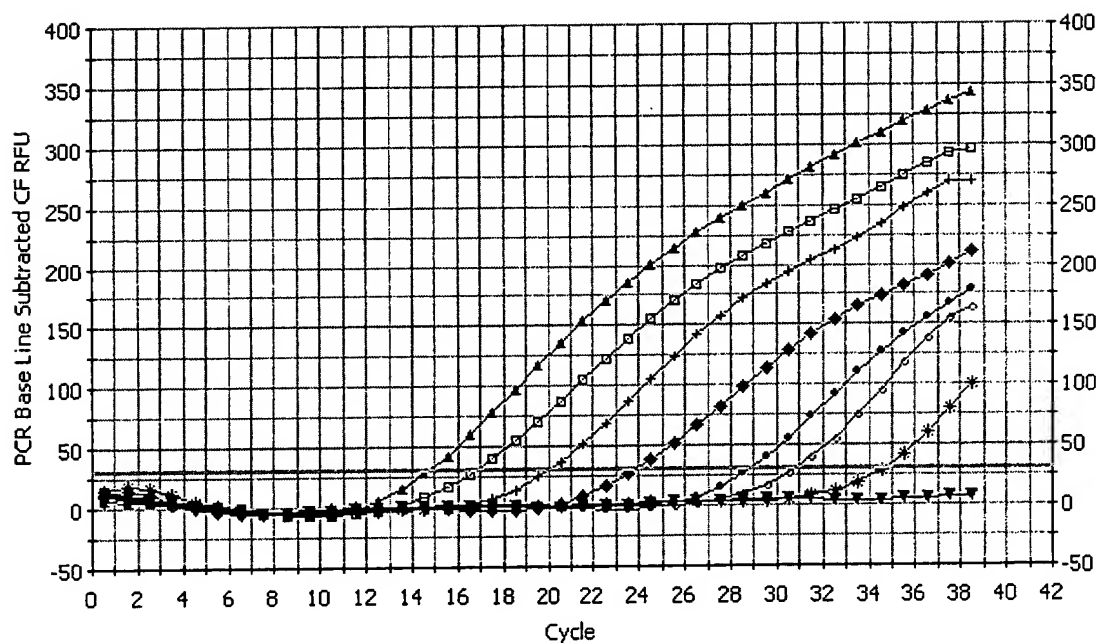
- 5 *A. acidoterrestris* ATCC 49025 (■) , *A. acidocaldarius* ATCC 43030 (□), 6 other bacteria under the detection baseline: *Bacillus subtilis* OSU 456, *Pseudomonas putida* 49L/51, *E. coli* DH5α , *Listeria monocytogenes* V7, *Lactococcus lactis* ML3 and *Geobacillus* ATCC 10149 ■ *Alicyclobacillus acidoterrestris* ATCC49025 ; □ *Alicyclobacillus acidocaldarius* ATCC43030; + *Bacillus subtilis* OSU456; ● *E. coli* DH5α; ▲ *Pseudomonas putida* 49L/51; ▼ *Geobacillus* ATCC 10149; ♦ *Lactococcus lactis* ML3 ; ○ *Listeria monocytogenes* V7

Figure 27



- 5 ▲ 1ml saline with 4×10^6 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml saline with 4×10^5 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- + 1ml saline with 4×10^4 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- ◆ 1ml saline with 4×10^3 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml saline with 4×10^2 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 10 ○ 1ml saline with 4×10^1 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- * 1ml saline with 4CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- ▼ 1ml saline

Figure 28



5

- ◆: 10^6 cells; □: 10^4 cells; ▼: 10^2 cells; ●: bacterial medium (blank) control.
- ▲ 1ml apple juice with 4×10^6 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml apple juice with 4×10^5 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- + 1ml apple juice with 4×10^4 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- ◆ 1ml apple juice with 4×10^3 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml apple juice with 4×10^2 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- 1ml apple juice with 4×10^1 CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025
- * 1ml apple juice with 4CFU/ml *Alicyclobacillus acidoterrestris* ATCC49025

15 ▼ 1ml apple Juice